

## SEQUENCE LISTING

Sequence No.: 1

Sequence length: 205

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP00442

## Sequence description

```

Met Thr Gly Leu Ala Leu Leu Tyr Ser Gly Val Phe Val Ala Phe Trp
 1              5              10              15
Ala Cys Ala Leu Ala Val Gly Val Cys Tyr Thr Ile Phe Asp Leu Gly
      20              25              30
Phe Arg Phe Asp Val Ala Trp Phe Leu Thr Glu Thr Ser Pro Phe Met
      35              40              45
Trp Ser Asn Leu Gly Ile Gly Leu Ala Ile Ser Leu Ser Val Val Gly
      50              55              60
Ala Ala Trp Gly Ile Tyr Ile Thr Gly Ser Ser Ile Ile Gly Gly Gly
      65              70              75              80
Val Lys Ala Pro Arg Ile Lys Thr Lys Asn Leu Val Ser Ile Ile Phe
      85              90              95
Cys Glu Ala Val Ala Ile Tyr Gly Ile Ile Met Ala Ile Val Ile Ser
      100             105             110
Asn Met Ala Glu Pro Phe Ser Ala Thr Asp Pro Lys Ala Ile Gly His
      115             120             125
Arg Asn Tyr His Ala Gly Tyr Ser Met Phe Gly Ala Gly Leu Thr Val
      130             135             140
Gly Leu Ser Asn Leu Phe Cys Gly Val Cys Val Gly Ile Val Gly Ser
      145             150             155             160
Gly Ala Ala Leu Ala Asp Ala Gln Asn Pro Ser Leu Phe Val Lys Ile
      165             170             175
Leu Ile Val Glu Ile Phe Gly Ser Ala Ile Gly Leu Phe Gly Val Ile
      180             185             190
Val Ala Ile Leu Gln Thr Ser Arg Val Lys Met Gly Asp
      195             200             205

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Sequence No.: 2

Sequence length: 371

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Leukocyte

Clone name: HP00804

Sequence description

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro  
 1 5 10 15  
 Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr  
 20 25 30  
 Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln  
 35 40 45  
 Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr  
 50 55 60  
 Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro  
 65 70 75 80  
 Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln  
 85 90 95  
 Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn  
 100 105 110  
 Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro  
 115 120 125  
 Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn  
 130 135 140  
 Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala  
 145 150 155 160  
 Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr  
 165 170 175  
 Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe  
 180 185 190  
 Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe  
 195 200 205  
 Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His  
 210 215 220  
 Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr  
 225 230 235 240  
 Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met  
 245 250 255

Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser  
 260 265 270  
 Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val  
 275 280 285  
 Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg  
 290 295 300  
 Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe  
 305 310 315 320  
 Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Gly Asn Lys Gln  
 325 330 335  
 Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr  
 340 345 350  
 Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg  
 355 360 365  
 Ala Lys Glu  
 370

Sequence No.: 3

Sequence length: 179

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP01098

Sequence description

Met Leu Ser Leu Asp Phe Leu Asp Asp Val Arg Arg Met Asn Lys Arg  
 1 5 10 15  
 Gln Leu Tyr Tyr Gln Val Leu Asn Phe Gly Met Ile Val Ser Ser Ala  
 20 25 30  
 Leu Met Ile Trp Lys Gly Leu Met Val Ile Thr Gly Ser Glu Ser Pro  
 35 40 45  
 Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala Phe His Arg Gly  
 50 55 60  
 Asp Leu Leu Phe Leu Thr Asn Arg Val Glu Asp Pro Ile Arg Val Gly  
 65 70 75 80  
 Glu Ile Val Val Phe Arg Ile Glu Gly Arg Glu Ile Pro Ile Val His  
 85 90 95  
 Arg Val Leu Lys Ile His Glu Lys Gln Asn Gly His Ile Lys Phe Leu  
 100 105 110

95

Thr Lys Gly Asp Asn Asn Ala Val Asp Asp Arg Gly Leu Tyr Lys Gln  
 115 120 125  
 Gly Gln His Trp Leu Glu Lys Lys Asp Val Val Gly Arg Ala Arg Gly  
 130 135 140  
 Phe Val Pro Tyr Ile Gly Ile Val Thr Ile Leu Met Asn Asp Tyr Pro  
 145 150 155 160  
 Lys Phe Lys Tyr Ala Val Leu Phe Leu Leu Gly Leu Phe Val Leu Val  
 165 170 175  
 His Arg Glu

Sequence No.: 4

Sequence length: 347

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01148

Sequence description

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
 1 5 10 15  
 Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
 20 25 30  
 Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
 35 40 45  
 Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
 50 55 60  
 Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
 65 70 75 80  
 Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
 85 90 95  
 Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
 100 105 110  
 Asp Cys Ser His Glu Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys

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	165		170		175
Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn					
	180		185		190
Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys					
	195		200		205
Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly					
	210		215		220
Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp					
	225		230		235
Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg					
	245		250		255
Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn					
	260		265		270
Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly					
	275		280		285
Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly					
	290		295		300
Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln					
	305		310		315
Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr					
	325		330		335
His Gln Glu Asp Val Ala Val Ile Cys Ser Gly					
	340		345		

Sequence No.: 5

Sequence length: 554

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01293

Sequence description

Met Pro Thr Val Asp Asp Ile Leu Glu Gln Val Gly Glu Ser Gly Trp			
1	5	10	15
Phe Gln Lys Gln Ala Phe Leu Ile Leu Cys Leu Leu Ser Ala Ala Phe			
20	25		30
Ala Pro Ile Cys Val Gly Ile Val Phe Leu Gly Phe Thr Pro Asp His			
35	40		45
His Cys Gln Ser Pro Gly Val Ala Glu Leu Ser Gln Arg Cys Gly Trp			

50				55				60							
Ser	Pro	Ala	Glu	Glu	Leu	Asn	Tyr	Thr	Val	Pro	Gly	Leu	Gly	Pro	Ala
65					70					75					80
Gly	Glu	Ala	Phe	Leu	Gly	Gln	Cys	Arg	Arg	Tyr	Glu	Val	Asp	Trp	Asn
				85					90						95
Gln	Ser	Ala	Leu	Ser	Cys	Val	Asp	Pro	Leu	Ala	Ser	Leu	Ala	Thr	Asn
				100				105					110		
Arg	Ser	His	Leu	Pro	Leu	Gly	Pro	Cys	Gln	Asp	Gly	Trp	Val	Tyr	Asp
		115					120					125			
Thr	Pro	Gly	Ser	Ser	Ile	Val	Thr	Glu	Phe	Asn	Leu	Val	Cys	Ala	Asp
		130			135						140				
Ser	Trp	Lys	Leu	Asp	Leu	Phe	Gln	Ser	Cys	Leu	Asn	Ala	Gly	Phe	Phe
145				150					155						160
Phe	Gly	Ser	Leu	Gly	Val	Gly	Tyr	Phe	Ala	Asp	Arg	Phe	Gly	Arg	Lys
				165				170						175	
Leu	Cys	Leu	Leu	Gly	Thr	Val	Leu	Val	Asn	Ala	Val	Ser	Gly	Val	Leu
				180				185					190		
Met	Ala	Phe	Ser	Pro	Asn	Tyr	Met	Ser	Met	Leu	Leu	Phe	Arg	Leu	Leu
		195					200					205			
Gln	Gly	Leu	Val	Ser	Lys	Gly	Asn	Trp	Met	Ala	Gly	Tyr	Thr	Leu	Ile
		210				215					220				
Thr	Glu	Phe	Val	Gly	Ser	Gly	Ser	Arg	Arg	Thr	Val	Ala	Ile	Met	Tyr
225				230					235						240
Gln	Met	Ala	Phe	Thr	Val	Gly	Leu	Val	Ala	Leu	Thr	Gly	Leu	Ala	Tyr
				245				250						255	
Ala	Leu	Pro	His	Trp	Arg	Trp	Leu	Gln	Leu	Ala	Val	Ser	Leu	Pro	Thr
			260				265						270		
Phe	Leu	Phe	Leu	Leu	Tyr	Tyr	Trp	Cys	Val	Pro	Glu	Ser	Pro	Arg	Trp
		275					280					285			
Leu	Leu	Ser	Gln	Lys	Arg	Asn	Thr	Glu	Ala	Ile	Lys	Ile	Met	Asp	His
		290				295					300				
Ile	Ala	Gln	Lys	Asn	Gly	Lys	Leu	Pro	Pro	Ala	Asp	Leu	Lys	Met	Leu
305				310					315						320
Ser	Leu	Glu	Glu	Asp	Val	Thr	Glu	Lys	Leu	Ser	Pro	Ser	Phe	Ala	Asp
				325				330						335	
Leu	Phe	Arg	Thr	Pro	Arg	Leu	Arg	Lys	Arg	Thr	Phe	Ile	Leu	Met	Tyr
		340					345					350			
Leu	Trp	Phe	Thr	Asp	Ser	Val	Leu	Tyr	Gln	Gly	Leu	Ile	Leu	His	Met
		355					360				365				
Gly	Ala	Thr	Ser	Gly	Asn	Leu	Tyr	Leu	Asp	Phe	Leu	Tyr	Ser	Ala	Leu
		370			375					380					
Val	Glu	Ile	Pro	Gly	Ala	P									

98

405 410 415  
 Cys Leu Val Met Ile Phe Ile Ser Pro Asp Leu His Trp Leu Asn Ile  
 420 425 430  
 Ile Ile Met Cys Val Gly Arg Met Gly Ile Thr Ile Ala Ile Gln Met  
 435 440 445  
 Ile Cys Leu Val Asn Ala Glu Leu Tyr Pro Thr Phe Val Arg Asn Leu  
 450 455 460  
 Gly Val Met Val Cys Ser Ser Leu Cys Asp Ile Gly Gly Ile Ile Thr  
 465 470 475 480  
 Pro Phe Ile Val Phe Arg Leu Arg Glu Val Trp Gln Ala Leu Pro Leu  
 485 490 495  
 Ile Leu Phe Ala Val Leu Gly Leu Leu Ala Ala Gly Val Thr Leu Leu  
 500 505 510  
 Leu Pro Glu Thr Lys Gly Val Ala Leu Pro Glu Thr Met Lys Asp Ala  
 515 520 525  
 Glu Asn Leu Gly Arg Lys Ala Lys Pro Lys Glu Asn Thr Ile Tyr Leu  
 530 535 540  
 Lys Val Gln Thr Ser Glu Pro Ser Gly Thr  
 545 550

Sequence No.: 6

Sequence length: 350

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10013

Sequence description

Met Ala Val Phe Val Val Leu Leu Ala Leu Val Ala Gly Val Leu Gly  
 1 5 10 15  
 Asn Glu Phe Ser Ile Leu Lys Ser Pro Gly Ser Val Val Phe Arg Asn  
 20 25 30  
 Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala Leu  
 35 40 45  
 Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala  
 50 55 60  
 Val Gly Asn Leu Phe His Arg Pro Arg Ala Thr Val Met Val Met Val  
 65 70 75 80

Lys Gly Val Asn Lys Leu Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr  
 85 90 95  
 Pro Leu Glu Asn Ala Val Pro Phe Ser Leu Asp Ser Val Ala Asn Ser  
 100 105 110  
 Ile His Ser Leu Phe Ser Glu Glu Thr Pro Val Val Leu Gln Leu Ala  
 115 120 125  
 Pro Ser Glu Glu Arg Val Tyr Met Val Gly Lys Ala Asn Ser Val Phe  
 130 135 140  
 Glu Asp Leu Ser Val Thr Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln  
 145 150 155 160  
 Glu Asn Ser Val Leu Ser Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn  
 165 170 175  
 Asn Glu Val Asp Leu Leu Phe Leu Ser Glu Leu Gln Val Leu His Asp  
 180 185 190  
 Ile Ser Ser Leu Leu Ser Arg His Lys His Leu Ala Lys Asp His Ser  
 195 200 205  
 Pro Asp Leu Tyr Ser Leu Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys  
 210 215 220  
 Arg Tyr Gly Glu Asp Ser Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu  
 225 230 235 240  
 Val Asp Ala Leu Gln Lys Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly  
 245 250 255  
 Gly Asn Ala Val Val Glu Leu Val Thr Val Lys Ser Phe Asp Thr Ser  
 260 265 270  
 Leu Ile Arg Lys Thr Arg Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn  
 275 280 285  
 Pro Ala Ser Pro Tyr Asn Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser  
 290 295 300  
 Val Val Phe Asn Met Val Leu Trp Ile Met Ile Ala Leu Ala Leu Ala  
 305 310 315 320  
 Val Ile Ile Thr Ser Tyr Asn Ile Trp Asn Met Asp Pro Gly Tyr Asp  
 325 330 335  
 Ser Ile Ile Tyr Arg Met Thr Asn Gln Lys Ile Arg Met Asp  
 340 345 350

Sequence No.: 7

Sequence length: 209

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*



100

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10034

Sequence description

```

Met Val Ser Ser Pro Cys Thr Gln Ala Ser Ser Arg Thr Cys Ser Arg
 1              5              10              15
Ile Leu Gly Leu Ser Leu Gly Thr Ala Ala Leu Phe Ala Ala Gly Ala
      20              25              30
Asn Val Ala Leu Leu Leu Pro Asn Trp Asp Val Thr Tyr Leu Leu Arg
      35              40              45
Gly Leu Leu Gly Arg His Ala Met Leu Gly Thr Gly Leu Trp Gly Gly
      50              55              60
Gly Leu Met Val Leu Thr Ala Ala Ile Leu Ile Ser Leu Met Gly Trp
      65              70              75              80
Arg Tyr Gly Cys Phe Ser Lys Ser Gly Leu Cys Arg Ser Val Leu Thr
      85              90              95
Ala Leu Leu Ser Gly Gly Leu Ala Leu Leu Gly Ala Leu Ile Cys Phe
      100             105             110
Val Thr Ser Gly Val Ala Leu Lys Asp Gly Pro Phe Cys Met Phe Asp
      115             120             125
Val Ser Ser Phe Asn Gln Thr Gln Ala Trp Lys Tyr Gly Tyr Pro Phe
      130             135             140
Lys Asp Leu His Ser Arg Asn Tyr Leu Tyr Asp Arg Ser Leu Trp Asn
      145             150             155             160
Ser Val Cys Leu Glu Pro Ser Ala Ala Val Val Trp His Val Ser Leu
      165             170             175
Phe Ser Ala Leu Leu Cys Ile Ser Leu Leu Gln Leu Leu Leu Val Val
      180             185             190
Val His Val Ile Asn Ser Leu Leu Gly Leu Phe Cys Ser Leu Cys Glu
      195             200             205

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Lys

Sequence No.: 8

Sequence length: 163

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

101

Clone name: HP10050

## Sequence description

```

Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala
 1           5           10           15
Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser
      20           25           30
Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro
      35           40           45
Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu
      50           55           60
Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro
      65           70           75           80
Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser
      85           90           95
Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr
      100          105          110
Arg Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu Trp Ser
      115          120          125
Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu
      130          135          140
Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro
      145          150          155          160
Glu Asp Glu

```

Sequence No.: 9

Sequence length: 92

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10071

## Sequence description

```

Met Thr Lys Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser
 1           5           10           15
Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu
      20           25           30
Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser
      35           40           45

```

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Met	Glu	Tyr	Leu	Ala	His	Pro	Ser	Thr	Leu	Gly	Leu	Ala	Val	Gly	Val
1				5					10					15	
Ala	Cys	Gly	Met	Cys	Leu	Gly	Trp	Ser	Leu	Arg	Val	Cys	Phe	Gly	Met
			20					25				30			
Leu	Pro	Lys	Ser	Lys	Thr	Ser	Lys	Thr	His	Thr	Asp	Thr	Glu	Ser	Glu
		35					40					45			
Ala	Ser	Ile	Leu	Gly	Asp	Ser	Gly	Glu	Tyr	Lys	Met	Ile	Leu	Val	Val
	50					55					60				
Arg	Asn	Asp	Leu	Lys	Met	Gly	Lys	Gly	Lys	Val	Ala	Ala	Gln	Cys	Ser
65					70					75					80
His	Ala	Ala	Val	Ser	Ala	Tyr	Lys	Gln	Ile	Gln	Arg	Arg	Asn	Pro	Glu
			85						90					95	
Met	Leu	Lys	Gln	Trp	Glu	Tyr	Cys	Gly	Gln	Pro	Lys	Val	Val	Val	Lys
			100					105					110		
Ala	Pro	Asp	Glu	Glu	Thr	Leu	Ile	Ala	Leu	Leu	Ala	His	Ala	Lys	Met
		115					120					125			
Leu	Gly	Leu	Thr	Val	Ser	Leu	Ile	Gln	Asp	Ala	Gly	Arg	Thr	Gln	Ile
	130					135					140				
Ala	Pro	Gly	Ser	Gln	Thr	Val	Leu	Gly	Ile	Gly	Pro	Gly	Pro	Ala	Asp
145					150					155					160
Leu	Ile	Asp	Lys	Val	Thr	Gly	His	Leu	Lys	Leu	Tyr				
				165					170						

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Sequence No.: 11  
 Sequence length: 149  
 Sequence type: Amino acid  
 Topology: Linear  
 Sequence kind: Protein  
 Hypothetical: No  
 Original source:  
   Organism species: *Homo sapiens*  
   Cell kind: Lymphoma  
   Cell line: U937  
   Clone name: HP10085  
 Sequence description

Met	Met	Thr	Lys	His	Lys	Lys	Cys	Phe	Ile	Ile	Val	Gly	Val	Leu	Ile	1	5	10	15
Thr	Thr	Asn	Ile	Ile	Thr	Leu	Ile	Val	Lys	Leu	Thr	Arg	Asp	Ser	Gln	20	25	30	
Ser	Leu	Cys	Pro	Tyr	Asp	Trp	Ile	Gly	Phe	Gln	Asn	Lys	Cys	Tyr	Tyr	35	40	45	
Phe	Ser	Lys	Glu	Glu	Gly	Asp	Trp	Asn	Ser	Ser	Lys	Tyr	Asn	Cys	Ser	50	55	60	
Thr	Gln	His	Ala	Asp	Leu	Thr	Ile	Ile	Asp	Asn	Ile	Glu	Glu	Met	Asn	65	70	75	80
Phe	Leu	Arg	Arg	Tyr	Lys	Cys	Ser	Ser	Asp	His	Trp	Ile	Gly	Leu	Lys	85	90	95	
Met	Ala	Lys	Asn	Arg	Thr	Gly	Gln	Trp	Val	Asp	Gly	Ala	Thr	Phe	Thr	100	105	110	
Lys	Ser	Phe	Gly	Met	Arg	Gly	Ser	Glu	Gly	Cys	Ala	Tyr	Leu	Ser	Asp	115	120	125	
Asp	Gly	Ala	Ala	Thr	Ala	Arg	Cys	Tyr	Thr	Glu	Arg	Lys	Trp	Ile	Cys	130	135	140	
Arg	Lys	Arg	Ile	His	145														

Sequence No.: 12  
 Sequence length: 188  
 Sequence type: Amino acid  
 Topology: Linear  
 Sequence kind: Protein  
 Hypothetical: No  
 Original source:  
   Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10122

## Sequence description

Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe Ile Ser Val  
 1 5 10 15  
 Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu Val Tyr Arg  
 20 25 30  
 Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys Gln Ser Lys  
 35 40 45  
 Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala Gly Arg Gln  
 50 55 60  
 Gln Lys Lys Lys Ile Glu Arg Gln Glu Glu Lys Leu Lys Asn Asn Asn  
 65 70 75 80  
 Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala Ile Gly Phe  
 85 90 95  
 Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe Asp Gly Arg  
 100 105 110  
 Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Tyr Ile Gln Gly Leu  
 115 120 125  
 Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys Ser Phe Ile  
 130 135 140  
 Phe Leu Tyr Ile Leu Cys Thr Met Ser Ile Arg Gln Asn Ile Gln Lys  
 145 150 155 160  
 Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln Ala Gly Gly  
 165 170 175  
 Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe Ser  
 180 185

Sequence No.: 13

Sequence length: 215

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10136

## Sequence description

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu

105

1	5	10	15
Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg Asp Leu Gln Gln			
20	25	30	
Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys Leu Asn Glu Gln Ser			
35	40	45	
Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met Thr Phe His Tyr Ile			
50	55	60	
Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys Glu Ala Ala Phe Pro			
65	70	75	80
Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu His Ser Glu Phe Asp			
85	90	95	
Glu Gln His Gly Lys Lys Val Pro Thr Val Ser Arg Pro Tyr Ser Phe			
100	105	110	
Ile Glu Phe Asp Thr Phe Ile Gln Lys Thr Lys Lys Leu Tyr Ile Asp			
115	120	125	
Ser Arg Ala Arg Arg Asn Leu Gly Ser Ile Asn Thr Glu Leu Gln Asp			
130	135	140	
Val Gln Arg Ile Met Val Ala Asn Ile Glu Glu Val Leu Gln Arg Gly			
145	150	155	160
Glu Ala Leu Ser Ala Leu Asp Ser Lys Ala Asn Asn Leu Ser Ser Leu			
165	170	175	
Ser Lys Lys Tyr Arg Gln Asp Ala Lys Tyr Leu Asn Met Arg Ser Thr			
180	185	190	
Tyr Ala Lys Leu Ala Ala Val Ala Val Phe Phe Ile Met Leu Ile Val			
195	200	205	
Tyr Val Arg Phe Trp Trp Leu			
210	215		

Sequence No.: 14

Sequence length: 112

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10175

Sequence description

Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly			
1	5	10	15
Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala			

106

20 25 30  
 Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala  
 35 40 45  
 Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val  
 50 55 60  
 Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe  
 65 70 75 80  
 Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser  
 85 90 95  
 Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His  
 100 105 110

Sequence No.: 15

Sequence length: 114

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10179

Sequence description

Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe  
 1 5 10 15  
 Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys  
 20 25 30  
 Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu  
 35 40 45  
 Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp  
 50 55 60  
 Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly Met  
 65 70 75 80  
 Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala Gly  
 85 90 95  
 Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met Thr  
 100 105 110  
 Ser Asp

Sequence No.: 16

Sequence length: 327

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10196

Sequence description

```

Met Ala Ala Ala Ala Ala Ala Ala Ala Thr Asn Gly Thr Gly Gly
 1             5             10             15
Ser Ser Gly Met Glu Val Asp Ala Ala Val Val Pro Ser Val Met Ala
      20             25             30
Cys Gly Val Thr Gly Ser Val Ser Val Ala Leu His Pro Leu Val Ile
      35             40             45
Leu Asn Ile Ser Asp His Trp Ile Arg Met Arg Ser Gln Glu Gly Arg
      50             55             60
Pro Val Gln Val Ile Gly Ala Leu Ile Gly Lys Gln Glu Gly Arg Asn
      65             70             75             80
Ile Glu Val Met Asn Ser Phe Glu Leu Leu Ser His Thr Val Glu Glu
      85             90             95
Lys Ile Ile Ile Asp Lys Glu Tyr Tyr Tyr Thr Lys Glu Glu Gln Phe
      100            105            110
Lys Gln Val Phe Lys Glu Leu Glu Phe Leu Gly Trp Tyr Thr Thr Gly
      115            120            125
Gly Pro Pro Asp Pro Ser Asp Ile His Val His Lys Gln Val Cys Glu
      130            135            140
Ile Ile Glu Ser Pro Leu Phe Leu Lys Leu Asn Pro Met Thr Lys His
      145            150            155            160
Thr Asp Leu Pro Val Ser Val Phe Glu Ser Val Ile Asp Ile Ile Asn
      165            170            175
Gly Glu Ala Thr Met Leu Phe Ala Glu Leu Thr Tyr Thr Leu Ala Thr
      180            185            190
Glu Glu Ala Glu Arg Ile Gly Val Asp His Val Ala Arg Met Thr Ala
      195            200            205
Thr Gly Ser Gly Glu Asn Ser Thr Val Ala Glu His Leu Ile Ala Gln
      210            215            220
His Ser Ala Ile Lys Met Leu His Ser Arg Val Lys Leu Ile Leu Glu
      225            230            235            240
Tyr Val Lys Ala Ser Glu Ala Gly Glu Val Pro Phe Asn His Glu Ile
      245            250            255

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Leu Arg Glu Ala Tyr Ala Leu Cys His Cys Leu Pro Val Leu Ser Thr  
                   260                                  265                                  270  
 Asp Lys Phe Lys Thr Asp Phe Tyr Asp Gln Cys Asn Asp Val Gly Leu  
                   275                                  280                                  285  
 Met Ala Tyr Leu Gly Thr Ile Thr Lys Thr Cys Asn Thr Met Asn Gln  
                   290                                  295                                  300  
 Phe Val Asn Lys Phe Asn Val Leu Tyr Asp Arg Gln Gly Ile Gly Arg  
                   305                                  310                                  315                                  320  
 Arg Met Arg Gly Leu Phe Phe  
   325

Sequence No.: 17

Sequence length: 373

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10235

Sequence description

Met Thr Leu Cys Ala Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu Asn  
   1                                  5                                  10                                  15  
 Ser Phe Leu His Gln Arg Ile Pro Gln Ser Val Arg Ile Leu Gly Ser  
                   20                                  25                                  30  
 Leu Val Ala Ile Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val Lys  
                   35                                  40                                  45  
 Val Gln Leu Asp Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys Ile  
                   50                                  55                                  60  
 Val Leu Ile Asn Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe Gly  
                   65                                  70                                  75                                  80  
 Leu Ala Gly Leu Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser Gly  
   85                                  90                                  95  
 Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala Ile  
                   100                                  105                                  110  
 Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile Thr  
                   115                                  120                                  125  
 Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu Pro  
                   130                                  135                                  140  
 Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly Pro

109

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145              150              155              160
Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu Pro
              165              170              175
Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln Pro
              180              185              190
Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser Val
              195              200              205
Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met Phe
              210              215              220
Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser Thr
225              230              235              240
Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn Ile
              245              250              255
Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro Gly
              260              265              270
Lys Asp Ser Arg Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val Phe
              275              280              285
Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu Thr
              290              295              300
Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala Phe
305              310              315              320
Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly Pro
              325              330              335
Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met Ala
              340              345              350
Phe Phe Leu Cys Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe Leu
              355              360              365
Phe Arg Ala Ile Val
              370

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Sequence No.: 18

Sequence length: 183

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10297

Sequence description

110

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro  
 1 5 10 15  
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile  
 20 25 30  
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val  
 35 40 45  
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val  
 50 55 60  
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr  
 65 70 75 80  
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu  
 85 90 95  
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val  
 100 105 110  
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn  
 115 120 125  
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser  
 130 135 140  
 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala  
 145 150 155 160  
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe  
 165 170 175  
 Asp Arg His Lys Met Leu Ser  
 180

Sequence No.: 19

Sequence length: 116

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10299

Sequence description

Met Ala Ser Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly  
 1 5 10 15  
 Phe Ala Gly Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Pro Gln  
 20 25 30  
 Val Lys Gln Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly  
 35 40 45

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Tyr Tyr Arg Gly Gly Phe Glu Pro Lys Met Thr Lys Arg Glu Ala Ala  
 50 55 60  
 Leu Ile Leu Gly Val Ser Pro Thr Ala Asn Lys Gly Lys Ile Arg Asp  
 65 70 75 80  
 Ala His Arg Arg Ile Met Leu Leu Asn His Pro Asp Lys Gly Gly Ser  
 85 90 95  
 Pro Tyr Ile Ala Ala Lys Ile Asn Glu Ala Lys Asp Leu Leu Glu Gly  
 100 105 110  
 Gln Ala Lys Lys  
 115

Sequence No.: 20

Sequence length: 152

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10301

Sequence description

Met Ala Val Leu Ser Lys Glu Tyr Gly Phe Val Leu Leu Thr Gly Ala  
 1 5 10 15  
 Ala Ser Phe Ile Met Val Ala His Leu Ala Ile Asn Val Ser Lys Ala  
 20 25 30  
 Arg Lys Lys Tyr Lys Val Glu Tyr Pro Ile Met Tyr Ser Thr Asp Pro  
 35 40 45  
 Glu Asn Gly His Ile Phe Asn Cys Ile Gln Arg Ala His Gln Asn Thr  
 50 55 60  
 Leu Glu Val Tyr Pro Pro Phe Leu Phe Phe Leu Ala Val Gly Gly Val  
 65 70 75 80  
 Tyr His Pro Arg Ile Ala Ser Gly Leu Gly Leu Ala Trp Ile Val Gly  
 85 90 95  
 Arg Val Leu Tyr Ala Tyr Gly Tyr Tyr Thr Gly Glu Pro Ser Lys Arg  
 100 105 110  
 Ser Arg Gly Ala Leu Gly Ser Ile Ala Leu Leu Gly Leu Val Gly Thr  
 115 120 125  
 Thr Val Cys Ser Ala Phe Gln His Leu Gly Trp Val Lys Ser Gly Leu  
 130 135 140  
 Gly Ser Gly Pro Lys Cys Cys His

145

150

Sequence No.: 21

Sequence length: 559

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP10302

Sequence description

Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg Trp Trp Met Ala  
1 5 10 15  
Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala Val Leu Leu Gly  
20 25 30  
Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly Phe Tyr Ser Ser  
35 40 45  
Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln Asp Glu Gln Arg  
50 55 60  
Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu Asn Leu Gly Phe  
65 70 75 80  
Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu Pro Leu Gly Ile  
85 90 95  
Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu Val Gly Ser Ala  
100 105 110  
Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala Ser Arg Asp Val  
115 120 125  
Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser Leu Asn Gly Phe  
130 135 140  
Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu Pro Asn Met Phe  
145 150 155 160  
Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile Gly Ser Tyr Ala  
165 170 175  
Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile Tyr Asp Ala Gly  
180 185 190  
Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly Leu Ala Cys Leu  
195 200 205  
Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu Ala Phe Pro Ala  
210 215 220  
Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu Ser Gly Leu Ala

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225                    230                    235                    240  
 Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr His Val Thr Thr  
                          245                    250                    255  
 Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu Glu Asp Gly Ser  
                          260                    265                    270  
 Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr Ser Glu Asn Leu  
                          275                    280                    285  
 Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys Ser Pro Thr Phe  
                          290                    295                    300  
 Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu Arg Ile Ile Phe  
 305                    310                    315                    320  
 Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu Val Thr Gly Gly  
                          325                    330                    335  
 Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val Ala Glu Thr Val  
                          340                    345                    350  
 Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu Leu Cys Leu Leu  
                          355                    360                    365  
 Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg Ile Lys Asp Cys  
                          370                    375                    380  
 Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp Ala Arg Asp Gly  
 385                    390                    395                    400  
 Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys Ile Gln Lys Leu  
                          405                    410                    415  
 Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu Leu Leu Val Gly  
                          420                    425                    430  
 Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu Gln Phe Val Thr  
                          435                    440                    445  
 Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His Ser Ala Cys Gly  
                          450                    455                    460  
 Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe Gly Thr Leu Thr  
 465                    470                    475                    480  
 Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu Leu Gln Gln Pro  
                          485                    490                    495  
 Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu Pro Phe Trp Val  
                          500                    505                    510  
 Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe Leu Leu Pro Ser  
                          515                    520                    525  
 Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu Tyr Ala Ala Asn  
                          530                    535                    540  
 Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu Val Thr Ala  
 545                    550                    555

Sequence length: 330

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Osteosarcoma

Cell line: U-2 OS

Clone name: HP10304

Sequence description

Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu Leu Leu Phe  
1 5 10 15  
Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala Pro Glu Pro  
20 25 30  
Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile Asn Val Thr  
35 40 45  
Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln Val Val Leu Asn  
50 55 60  
Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn Asp Leu Pro Val Asn  
65 70 75 80  
Ser Gly Val Thr Arg Ile Ser Cys Gln Thr Leu Ile Val Lys Asn Glu  
85 90 95  
Asn Leu Glu Asn Leu Glu Glu Lys Glu Tyr Phe Gly Ile Val Ser Val  
100 105 110  
Arg Ile Leu Val His Glu Trp Pro Met Thr Ser Gly Ser Ser Leu Gln  
115 120 125  
Leu Ile Val Ile Gln Glu Glu Val Val Glu Ile Asp Gly Lys Gln Val  
130 135 140  
Gln Gln Lys Asp Val Thr Glu Ile Asp Ile Leu Val Lys Asn Arg Gly  
145 150 155 160  
Val Leu Arg His Ser Asn Tyr Thr Leu Pro Leu Glu Glu Ser Met Leu  
165 170 175  
Tyr Ser Ile Ser Arg Asp Ser Asp Ile Leu Phe Thr Leu Pro Asn Leu  
180 185 190  
Ser Lys Lys Glu Ser Val Ser Ser Leu Gln Thr Thr Ser Gln Tyr Leu  
195 200 205  
Ile Arg Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu Pro Gly Lys  
210 215 220  
Leu Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser Tyr Lys Val  
225 230 235 240  
Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys Arg Phe Trp  
245 250 255

115

Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile Met Val Val  
 260 265 270  
 Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys Val Phe Phe  
 275 280 285  
 Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp Lys Val Asp Val  
 290 295 300  
 Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp Gly Pro Glu Lys Arg  
 305 310 315 320  
 Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile  
 325 330

Sequence No.: 23

Sequence length: 108

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Osteosarcoma

Cell line: HU-2 OS

Clone name: HP10305

Sequence description

Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala  
 1 5 10 15  
 Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys  
 20 25 30  
 Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His  
 35 40 45  
 Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp  
 50 55 60  
 Leu Gly Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe  
 65 70 75 80  
 Pro Phe Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp  
 85 90 95  
 Asn Val Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr  
 100 105

Sequence No.: 24

Sequence length: 101

Sequence type: Amino acid



116

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Osteosarcoma

Cell line: U-2 OS

Clone name: HP10306

Sequence description

```

Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
 1             5             10             15
Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
      20             25             30
Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
      35             40             45
Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
      50             55             60
Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
      65             70             75             80
Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile
      85             90             95
Pro Leu Gly Thr Pro
      100

```

Sequence No.: 25

Sequence length: 372

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10328

Sequence description

```

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
 1             5             10             15
Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
      20             25             30
Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala

```

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35 40 45  
 Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn  
 50 55 60  
 Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val  
 65 70 75 80  
 Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln  
 85 90 95  
 Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val  
 100 105 110  
 Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg  
 115 120 125  
 Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu Gln Leu Arg Leu Leu  
 130 135 140  
 Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu Ala Arg Lys Val Asn  
 145 150 155 160  
 Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly Asp Ile Leu Gln Trp  
 165 170 175  
 Asp Phe His Asp Ser Phe Phe Asn Leu Thr Leu Lys Gln Val Leu Phe  
 180 185 190  
 Leu Gln Trp Gln Glu Thr Arg Cys Ala Asn Ala Ser Phe Val Leu Asn  
 195 200 205  
 Gly Asp Asp Asp Val Phe Ala His Thr Asp Asn Met Val Phe Tyr Leu  
 210 215 220  
 Gln Asp His Asp Pro Gly Arg His Leu Phe Val Gly Gln Leu Ile Gln  
 225 230 235 240  
 Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr Val Pro Glu  
 245 250 255  
 Val Val Thr Gln Asn Glu Arg Tyr Pro Pro Tyr Cys Gly Gly Gly Gly  
 260 265 270  
 Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu Arg Arg Ala Ala His  
 275 280 285  
 Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe Leu Gly Met Cys Leu  
 290 295 300  
 Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile Arg Thr Ser  
 305 310 315 320  
 Gly Val Arg Ala Pro Ser Gln His Leu Ser Ser Phe Asp Pro Cys Phe  
 325 330 335  
 Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu  
 340 345 350  
 Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln  
 355 360 365  
 Thr Gln Ile Tyr  
 370

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Sequence No.: 26  
Sequence length: 615  
Sequence type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Sequence kind: cDNA to mRNA  
Original source:  
Organism species: *Homo sapiens*  
Cell kind: Fibrosarcoma  
Cell line: HT-1080  
Clone name: HP00442

## Sequence description

ATGACGGGGC TAGCACTGCT CTACTCCGGG GTCTTCGTGG CCTTCTGGGC CTGCGCGCTG	60
GCCGTGGGAG TCTGCTACAC CATT TTTGAT TTGGGCTTCC GCTTTGATGT GGCATGGTTC	120
CTGACGGAGA CTTCGCCCTT CATGTGGTCC AACCTGGGCA TTGGCCTAGC TATCTCCCTG	180
TCTGTGGTTG GGGCAGCCTG GGGCATCTAT ATTACGGGCT CCTCCATCAT TGGTGGAGGA	240
GTGAAGGCCC CCAGGATCAA GACCAAGAAC CTGGTCAGCA TCATCTTCTG TGAGGCTGTG	300
GCCATCTACG GCATCATCAT GGCAATTGTC ATTAGCAACA TGGCTGAGCC TTTCACTGCC	360
ACAGACCCCA AGGCCATCGG CCATCGGAAC TACCATGCAG GCTACTCCAT GTTTGGGGCT	420
GGCCTCACCG TAGGCCTGTC TAACCTCTTC TGTGGAGTCT GCGTGGGCAT CGTGGGCAGT	480
GGGGCTGCCC TGGCCGATGC TCAGAACCCC AGCCTCTTTG TAAAGATTCT CATCGTGGAG	540
ATCTTTGGCA GCGCCATTGG CCTCTTTGGG GTCATCGTCC CAATTCTTCA GACCTCCAGA	600
GTGAAGATGG GTGAC	615

Sequence No.: 27  
Sequence length: 1113  
Sequence type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Sequence kind: cDNA to mRNA  
Original source:  
Organism species: *Homo sapiens*  
Cell kind: Leukocyte  
Clone name: HP00804  
Sequence description

ATGTCCCATG AAAAGAGTTT TTTGGTGTCT GGGGACAACT ATCCTCCCCC CAACCCTGGA	60
TATCCGGGGG GGCCCCAGCC ACCCATGCCC CCCTATGCTC AGCCTCCCTA CCCTGGGGCC	120
CCTTACCCAC AGCCCCCTTT CCAGCCCTCC CCCTACGGTC AGCCAGGGTA CCCCCATGGC	180
CCCAGCCCCCT ACCCCCAAGG GGGCTACCCA CAGGGTCCCT ACCCCCAAGG GGGCTACCCA	240
CAGGGCCCCCT ACCCACAAGA GGGCTACCCA CAGGGCCCCCT ACCCCCAAGG GGGCTACCCC	300

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CAGGGGGCCAT ATCCCCAGAG CCCCTTCCCC CCCAACCCT ATGGACAGCC ACAGGTCTTC 360  
CCAGGACAAG ACCCTGACTC ACCCCAGCAT GGAACTACC AGGAGGAGGG TCCCCCATCC 420  
TACTATGACA ACCAGGACTT CCCTGCCACC AACTGGGATG ACAAGAGCAT CCGACAGGCC 480  
TTCATCCGCA AGGTGTTCTT AGTGCTGACC TTGCAGCTGT CCGTGACCCT GTCCACGGTG 540  
TCTGTGTTCA CTTTGTGTC GGAGGTGAAG GGCTTTGTCC GGGAGAATGT CTGGACCTAC 600  
TATGTCTCCT ATGCTGTCTT CTTCACTCTT CTCATCGTCC TCAGCTGTTG TGGGGACTTC 660  
CGGCGAAAAG ACCCCTGGAA CCTTGTGTC CTGTCGGTCC TGACCGCCAG CCTGTCTGAC 720  
ATGGTGGGGA TGATCGCCAG CTTCTACAAC ACCGAGGCAG TCATCATGGC CGTGGGCATC 780  
ACCACAGCCG TCTGCTTCAC CGTCGTATC TTCTCCATGC AGACCCGCTA CGACTTCACC 840  
TCATGCATGG GCGTGCTCCT GGTGAGCATG GTGGTGCTCT TCATCTTCGC CATTCTCTGC 900  
ATCTTCATCC GGAACCGCAT CCTGGAGATC GTGTACGCCCT CACTGGGCGC TCTGCTCTTC 960  
ACCTGCTTCC TCGCAGTGGA CACCCAGCTG CTGCTGGGGA ACAAGCAGCT GTCCCTGAGC 1020  
CCAGAAGAGT ATGTGTTTGC TCGCTGAAC CTGTACACAG ACATCATCAA CATCTTCCTG 1080  
TACATCCTCA CCATCATTGG CCGCGCCAAG GAG 1113

Sequence No.: 28

Sequence length: 537

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP01098

Sequence description

ATGCTGTCTC TAGACTTTTT GGACGATGTG CGGCGGATGA ACAAGCGGCA GCTCTATTAT 60  
CAAGTCTTAA ATTTTGAAT GATTGTCTCA TCGGCACTAA TGATCTGGAA GGGGTTAATG 120  
GTAATAACTG GAAGTGAAG TCCGATTGTA GTGGTGCTCA GTGGCAGCAT GGAACCTGCA 180  
TTTCATAGAG GAGATCTTCT CTTTCTAACA AATCGAGTTG AAGATCCCAT ACGAGTGGGA 240  
GAAATTGTTG TTTTATAGAT AGAAGGAAGA GAGATTCCTA TAGTTCACCG AGTCTTGAAG 300  
ATTCATGAAA AGCAAAATGG GCATATCAAG TTTTGGACCA AAGGAGATAA TAATGCGGTT 360  
GATGACCGAG GCCTCTATAA ACAAGGACAA CATTGGCTAG AGAAAAAGA TGTGTGGGG 420  
AGAGCCAGGG GATTTGTTCC TTATATTGGA ATTGTGACGA TCCTCATGAA TGACTATCCT 480  
AAATTAAAGT ATGCAGTTCT CTTTTTGCTG GGTATTTCG TGCTGGTTCA TCGTGAG 537

Sequence No.: 29

Sequence length: 1041

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01148

Sequence description

ATGGCTCTGC TATTCTCCTT GATCCTTGCC ATTTGCACCA GACCTGGATT CCTAGCGTCT 60  
CCATCTGGAG TCGGCTGGT GGGGGCCTC CACCGCTGTG AAGGGCGGT GGAGGTGGAA 120  
CAGAAAGGCC AGTGGGGCAC CGTGTGTGAT GACGGCTGGG ACATTAAGGA CGTGGCTGTG 180  
TTGTGCCGGG AGCTGGGCTG TGGAGCTGCC AGCGGAACCC CTAGTGGTAT TTTGTATGAG 240  
CCACCAGCAG AAAAAGAGCA AAAGGTCCTC ATCCAATCAG TCAGTTGCAC AGGAACAGAA 300  
GATACATTGG CTCAGTGTGA GCAAGAAGAA GTTTATGATT GTTCACATGA AGAAGATGCT 360  
GGGGCATCGT GTGAGAACCC AGAGAGCTCT TTCTCCCCAG TCCCAGAGGG TGTCAGGCTG 420  
GCTGACGGCC CTGGGCATTG CAAGGGACGC GTGGAAGTGA AGCACCAGAA CCAGTGGTAT 480  
ACCGTGTGCC AGACAGGCTG GAGCCTCCGG GCCGCAAAGG TGGTGTGCCG GCAGCTGGGA 540  
TGTGGGAGGG CTGTACTGAC TCAAAAACGC TGCAACAAGC ATGCCTATGG CCGAAAACCC 600  
ATCTGGCTGA GCCAGATGTC ATGCTCAGGA CGAGAAGCAA CCCTTCAGGA TTGCCCTTCT 660  
GGGCCTTGGG GGAAGAACAC CTGCAACCAT GATGAAGACA CGTGGGTCTGA ATGTGAAGAT 720  
CCCTTTGACT TGAGACTAGT AGGAGGAGAC AACCTCTGCT CTGGGCGACT GGAGGTGCTG 780  
CACAAGGGCG TATGGGGCTC TGTCTGTGAT GACAACTGGG GAGAAAAGGA GGACCAGGTG 840  
GTATGCAAGC AACTGGGCTG TGGGAAGTCC CTCTCTCCCT CCTTCAGAGA CCGGAAATGC 900  
TATGGCCCTG GGGTTGGCCG CATCTGGCTG GATAATGTTT GTTGCTCAGG GGAGGAGCAG 960  
TCCCTGGAGC AGTGCCAGCA CAGATTTTGG GGGTTTCACG ACTGCACCCA CCAGGAAGAT 1020  
GTGGCTGTCA TCTGCTCAGG A 1041

Sequence No.: 30

Sequence length: 1662

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01293

Sequence description

ATGCCCACCG TGGATGACAT TCTGGAGCAG GTTGGGGAGT CTGGCTGGTT CCAGAAGCAA 60  
GCCTTCTCA TCTTATGCCT GCTGTGGCT GCCTTTGCGC CCATCTGTGT GGGCATCGTC 120  
TTCCTGGGTT TCACACCTGA CCACCACTGC CAGAGTCTG GGGTGGCTGA GCTGAGCCAG 180  
CGCTGTGGCT GGAGCCCTGC GGAGGAGCTG AACTATACAG TGCCAGGCCT GGGGCCCCGC 240  
GGCGAGGCCT TCCTTGGCCA GTGCAGGCGC TATGAAAGTGG ACTGGAACCA GAGCGCCCTC 300

AGCTGTGTAG	ACCCCTGGC	TAGCCTGGCC	ACCAACAGGA	GCCACCTGCC	GCTGGGTCCC	360
TGCCAGGATG	GCTGGGTGTA	TGACACGCCC	GGCTCTTCCA	TCGTCACTGA	GTTCAACCTG	420
GTGTGTGCTG	ACTCCTGGAA	GCTGGACCTC	TTTCAGTCCT	GTTTGAATGC	GGGCTTCTTC	480
TTTGGCTCTC	TCGGTGTGG	CTACTTTGCA	GACAGGTTTG	GCCGTAAGCT	GTGTCTCCTG	540
GGAAGTGTGC	TGGTCAACGC	GGTGTGGGGC	GTGCTCATGG	CCTTCTCGCC	CAACTACATG	600
TCCATGCTGC	TCTTCCGCCT	GCTGCAGGGC	CTGGTCAGCA	AGGGCAACTG	GATGGCTGGC	660
TACACCCTAA	TCACAGAATT	TGTTGGCTCG	GGCTCCAGAA	GAACGGTGGC	GATCATGTAC	720
CAGATGGCCT	TCACGGTGGG	GCTGGTGGCG	CTTACCGGGC	TGGCCTACGC	CCTGCCTCAC	780
TGGCGCTGGC	TGCAGCTGGC	AGTCTCCCTG	CCCACCTTCC	TCTTCCTGCT	CTACTACTGG	840
TGTGTGCCGG	AGTCCCCTCG	GTGGCTGTTA	TCACAAAAAA	GAAACACTGA	AGCAATAAAG	900
ATAATGGACC	ACATCGCTCA	AAAGAATGGG	AAGTTGCCTC	CTGCTGATTT	AAAGATGCTT	960
TCCCTCGAAG	AGGATGTCAC	CGAAAAGCTG	AGCCCTTCAT	TTGCAGACCT	GTTCCGCACG	1020
CCGCGCCTGA	GGAAGCGCAC	CTTCATCCTG	ATGTACCTGT	GGTTCACGGA	CTCTGTGCTC	1080
TATCAGGGGC	TCATCCTGCA	CATGGGCGCC	ACCAGCGGGA	ACCTCTACCT	GGATTTCTTT	1140
TACTCCGCTC	TGGTCGAAAT	CCCGGGGGCC	TTCATAGCCC	TCATCACCAT	TGACCGCGTG	1200
GGCCGCATCT	ACCCCATGGC	CGTGTCAAAT	TTGTTGGCGG	GGGCAGCCTG	CCTCGTCATG	1260
ATTTTTATCT	CACCTGACCT	GCACTGGTTA	AACATCATAA	TCATGTGTGT	TGGCCGAATG	1320
GGAATCACCA	TTGCAATACA	AATGATCTGC	CTGGTGAATG	CTGAGCTGTA	CCCCACATTC	1380
GTCAGGAACC	TCGGAGTGAT	GGTGTGTTCC	TCCCTGTGTG	ACATAGGTGG	GATAATCACC	1440
CCCTTCATAG	TCTTCAGGCT	GAGGGAGGTC	TGGCAAGCCT	TGCCCCTCAT	TTTGTGTTGG	1500
GTGTTGGGCC	TGCTTGCCGC	GGGAGTGACG	CTACTTCTTC	CAGAGACCAA	GGGGGTGCGT	1560
TTGCCAGAGA	CCATGAAGGA	CGCCGAGAAC	CTTGGGAGAA	AAGCAAAGCC	CAAAGAAAAC	1620
ACGATTIACC	TTAAGGTCCA	AACCTCAGAA	CCCTCGGGCA	CC		1662

Sequence No.: 31

Sequence length: 1050

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10013

Sequence description

ATGGCTGTGT	TTGTCTGTCT	CCTGGCGTTG	GTGGCGGGTG	TTTTGGGGAA	CGAGTTTAGT	60
ATATTAAAAT	CACCAGGGTC	TGTTGTTTTT	CGAAATGGAA	ATTGGCCTAT	ACCAGGAGAG	120
CGGATCCCAG	ACGTGGCTGC	ATTGTCCATG	GGCTTCTCTG	TGAAAGAAGA	CCTTCTTGG	180
CCAGGACTCG	CAGTGGGTAA	CCTGTTTCAT	CGTCTCGGG	CTACCGTCAT	GGTGATGGTG	240
AAGGGAGTGA	ACAAACTGGC	TCTACCCCCA	GGCAGTGTCA	TTTCGTACCC	TTTGGAGAAT	300
GCAGTTCCTT	TTAGTCTTGA	CAGTGTGCA	AATTCCATTG	ACTCCTTATT	TTCTGAGGAA	360

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ACTCCTGTTG	TTTTGCAGTT	GGCTCCCAGT	GAGGAAAGAG	TGTATATGGT	AGGGAAGGCA	420
AACTCAGTGT	TTGAAGACCT	TTCAGTCACC	TTGCGCCAGC	TCCGTAATCG	CCTGTTTCAA	480
GAAAACTCTG	TTCTCAGTTC	ACTCCCCCTC	AATTCTCTGA	GTAGGAACAA	TGAAGTTGAC	540
CTGCTCTTTT	TTTCTGAACT	GCAAGTGCTA	CATGATATTT	CAAGCTTGCT	GTCTCGTCAT	600
AAGCATCTAG	CCAAGGATCA	TTCTCCTGAT	TTATATTAC	TGGAGCTGGC	AGGTTTGGAT	660
GAAATTGGGA	AGCGTTATGG	GGAAGACTCT	GAACAATTCA	GAGATGCTTC	TAAGATCCTT	720
GTTGACGCTC	TGCAAAAGTT	TGCAGATGAC	ATGTACAGTC	TTTATGGTGG	GAATGCAGTG	780
GTAGAGTTAG	TCACTGTCAA	GTCATTTGAC	ACCTCCCTCA	TTAGGAAGAC	AAGGACTATC	840
CTTGAGGCAA	AACAAGCGAA	GAACCCAGCA	AGTCCCTATA	ACCTTGcata	TAAGTATAAT	900
TTTGAATATT	CCGTGGTTTT	CAACATGGTA	CTTTGGATAA	TGATCGCCTT	GGCCTTGGCT	960
GTGATTATCA	CCTCTTACAA	TATTTGGAAC	ATGGATCCTG	GATATGATAG	CATCATTTAT	1020
AGGATGACAA	ACCAGAAGAT	TCGAATGGAT				1050

Sequence No.: 32

Sequence length: 627

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10034

Sequence description

ATGGTGTCTT	CTCCCTGCAC	GCAGGCAAGC	TCACGGACTT	GCTCCCGTAT	CCTGGGACTG	60
AGCCTTGGGA	CTGCAGCCCT	GTTTGCTGCT	GGGGCCAACG	TGGCACTCCT	CCTTCCTAAC	120
TGGGATGTCA	CCTACCTGTT	GAGGGGCCTC	CTTGGCAGGC	ATGCCATGCT	GGGAACTGGG	180
CTCTGGGGAG	GAGGCCTCAT	GGTACTCACT	GCAGCTATCC	TCATCTCCTT	GATGGGCTGG	240
AGATACGGCT	GCTTCAGTAA	GAGTGGGCTC	TGTCGAAGCG	TGCTTACTGC	TCTGTTGTCA	300
GGTGGCCTGG	CTTTACTTGG	AGCCCTGATT	TGCTTTGTCA	CTTCTGGAGT	TGCTCTGAAA	360
GATGGTCCTT	TTTGCATGTT	TGATGTTTCA	TCCTTCAATC	AGACACAAGC	TTGGAAATAT	420
GGTTACCCAT	TCAAAGACCT	GCATAGTAGG	AATTATCTGT	ATGACCGTTC	GCTCTGGAAC	480
TCCGTCTGCC	TGGAGCCCTC	TGCAGCTGTT	GTCTGGCAGC	TGTCCCTCTT	CTCCGCCCTT	540
CTGTGCATCA	GCCTGCTCCA	GCTTCTCCTG	GTGGTCGTTT	ATGTCATCAA	CAGCCTCCTG	600
GGCCTTTTCT	GCAGCCTCTG	CGAGAAG				627

Sequence No.: 33

Sequence length: 489

Sequence type: Nucleic acid

Strandedness: Double

WO 98/21328

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Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10050

Sequence description

```
ATGGCGGCTG GGCTGTTTGG TTTGAGCGCT CGCCGTCTTT TGGCGGCAGC GGCGACGCGA 60
GGGCTCCCCG CCGCCCGCGT CCGCTGGGAA TCTAGCTTCT CCAGGACTGT GGTGCCCCCG 120
TCCGCTGTGG CGGGAAAGCG GCCCCCAGAA CCGACCACAC CGTGGCAAGA GGACCCAGAA 180
CCCAGGACG AAAACTTGTA TGAGAAGAAC CCAGACTCCC ATGGTTATGA CAAGGACCCC 240
GTTTTGGACG TCTGGAACAT GCGACTTGTC TTCTTCTTTG GCGTCTCCAT CATCCTGCTC 300
CTTGGCAGCA CCTTTGTGGC CTATCTGCCT GACTACAGGT GCACAGGGTG TCCAAGAGCG 360
TGGGATGGGA TGAAAGAGTG GTCCCCCGC GAAGCTGAGA GGCTTGTGAA ATACCGAGAG 420
GCCAATGGCC TTCCCATCAT GGAATCCAAC TGCTTCGACC CCAGCAAGAT CCAGCTGCCA 480
GAGGATGAG 489
```

Sequence No.: 34

Sequence length: 276

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10071

Sequence description

```
ATGACGAAAT TAGCGCAGTG GCTTTGGGGA CTAGCGATCC TGGGCTCCAC CTGGGTGGCC 60
CTGACCACGG GAGCCTTGGG CCTGGAGCTG CCCTTGTCTT GCCAGGAAGT CCTGTGGCCA 120
CTGCCCCGCT ACTTGCTGGT GTCCGCCGCG TGCTATGCCC TGGGCACTGT GGGCTATCGT 180
GTGGCCACTT TTCATGACTG CGAGGACGCC GCACGCGAGC TGCAGAGCCA GATACAGGAG 240
GCCCCGAGCCG ACTTAGCCCC CAGGGGGCTG CGCTTC 276
```

Sequence No.: 35

Sequence length: 516

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear



Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10076

Sequence description

ATGGAATATT	TGGCTCATCC	CAGTACACTC	GGCTTGGCTG	TTGGAGTTGC	TTGTGGCATG	60
TGCCTGGGCT	GGAGCCTTCG	AGTATGCTTT	GGGATGCTCC	CCAAAAGCAA	GACGAGCAAG	120
ACACACACAG	ATACTGAAAG	TGAAGCAAGC	ATCTTGGGAG	ACAGCGGGGA	GTACAAGATG	180
ATTCTTGTGG	TTCGAAATGA	CTTAAAGATG	GGAAAAGGGA	AAGTGGCTGC	CCAGTGCTCT	240
CATGCTGCTG	TTTCAGCCTA	CAAGCAGATT	CAAAGAAGAA	ATCCTGAAAT	GCTCAAACAA	300
TGGGAATACT	GTGGCCAGCC	CAAGGTGGTG	GTCAAAGCTC	CTGATGAAGA	AACCCTGATT	360
GCATTATTGG	CCCATGCAAA	AATGCTGGGA	CTGACTGTAA	GTTTAATTCA	AGATGCTGGA	420
CGTACTCAGA	TTGCACCAGG	CTCTCAAAC	GTCTAGGGA	TTGGGCCAGG	ACCAGCAGAC	480
CTAATTGACA	AAGTCACTGG	TCACCTAAAA	CTTTAC			516

Sequence No.: 36

Sequence length: 447

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10085

Sequence description

ATGATGACCA	AACATAAAAA	GTGTTTTATA	ATTGTTGGTG	TTTAAATAAC	AACTAATATT	60
ATTACTCTGA	TAGTTAAACT	AACTCGAGAT	TCTCAGAGTT	TATGCCCTTA	TGATTGGATT	120
GGTTTCCAAA	ACAAATGCTA	TTATTTCTCT	AAAGAAGAAG	GAGATTGGAA	TTCAAGTAAA	180
TACAACTGTT	CCACTCAACA	TGCCGACCTA	ACTATAATTG	ACAACATAGA	AGAAATGAAT	240
TTTCTTAGGC	GGTATAAATG	CAGTTCTGAT	CACTGGATTG	GACTGAAGAT	GGCAAAAAAT	300
CGAACAGGAC	AATGGGTAGA	TGGAGCTACA	TTTACCAAAT	CGTTTGGCAT	GAGAGGGAGT	360
GAAGGATGTG	CCTACCTCAG	CGATGATGGT	GCAGCAACAG	CTAGATGTTA	CACCGAAAGA	420
AAATGGATTT	GCAGGAAAAG	AATACAC				447

Sequence No.: 37

Sequence length: 564

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10122

Sequence description

ATGAGCACTA	TGTTGCGGGA	CACTCTCCTC	ATCGTTTTTA	TCTCTGTGTG	CACGGCTCTG	60
CTGCGAGAGG	GCATAACCTG	GGTCCTGGTT	TACAGGACAG	ACAAGTACAA	GAGACTGAAG	120
GCAGAAGTGG	AAAAACAGAG	TAAAAAATTG	GAAAAGAAGA	AGGAAACAAT	AACAGAGTCA	180
GCTGGTCGAC	AACAGAAAAA	GAAAATAGAG	AGACAAGAAG	AGAAACTGAA	GAATAACAAC	240
AGAGATCTAT	CAATGGTTTCG	AATGAAATCC	ATGTTTGCTA	TTGGCTTTTG	TTTTACTGCC	300
CTAATGGGAA	TGTTCAATTC	CATATTTGAT	GGTAGAGTGG	TGGCAAAGCT	TCCTTTTACC	360
CCTCTTTCTT	ACATCCAAGG	ACTGTCTCAT	CGAAATCTGC	TGGGAGATGA	CACCACAGAC	420
TGTTCCTTCA	TTTTCTGTGA	TATTCTCTGT	ACTATGTCTG	TTCGACAGAA	CATTGAGAAG	480
ATTCTCGGCC	TTGCCCTTTC	ACGAGCCGCC	ACCAAGCAGG	CAGGTGGATT	TCTTGGCCCA	540
CCACCTCCTT	CTGGGAAGTT	CTCT				564

Sequence No.: 38

Sequence length: 645

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10136

Sequence description

ATGGTGTTC	TAACAATGAT	CGCCCGAGTG	GCGGACGGGC	TCCCGCTGGC	CGCCTCGATG	60
CAGGAGGACG	AACAGTCTGG	CCGGGACCTT	CAACAGTATC	AGAGTCAGGC	TAAGCAACTC	120
TTTCGAAAGT	TGAATGAACA	GTCCCCTACC	AGATGTACCT	TGGAAGCAGG	AGCCATGACT	180
TTTCACTACA	TTATTGAGCA	GGGGGTGTGT	TATTTGGTTT	TATGTGAAGC	TGCCTTCCCT	240
AAGAAGTTGG	CTTTTGCTTA	CCTAGAAGAT	TTGCACTCAG	AATTTGATGA	ACAGCATGGA	300
AAGAAGGTGC	CCACTGTGTC	CCGACCTTAT	TCCTTTATTG	AATTTGATAC	TTTCATTGAG	360
AAAACCAAGA	AGCTCTACAT	TGACAGTCGT	GCTCGAAGAA	ATCTAGGCTC	CATCAACACT	420
GAATTGCAAG	ATGTGCAGAG	GATCATGGTG	GCCAATATTG	AAGAAGTGTT	ACAACGAGGA	480
GAAGCACTCT	CAGCATTGGA	TTCAAAGGCT	AACAATTTGT	CCAGTCTGTC	CAAGAAATAC	540

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CGCCAGGATG CGAAGTACTT GAACATGCGT TCCACTTATG CCAAAGTTGC AGCAGTAGCT 600  
GTATTTTCA TCATGTAAAT AGTGTATGTC CGATTCTGGT GGCTG 645

Sequence No.: 39  
Sequence length: 336  
Sequence type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Sequence kind: cDNA to mRNA  
Original source:  
Organism species: *Homo sapiens*  
Cell kind: Stomach cancer  
Clone name: HP10175  
Sequence description

ATGCAGGACA CTGGCTCAGT AGTGCCTTTG CATTGGTTTG GCTTTGGCTA CGCAGCACTG 60  
GTTGCTTCTG GTGGGATCAT TGGCTATGTA AAAGCAGGCA GCGTGCCGTC CCTGGCTGCA 120  
GGGCTGCTCT TTGGCAGTCT AGCCGGCCTG GGTGCTTACC AGCTGTCTCA GGATCCAAGG 180  
AACGTTTGGG TTTTCCTAGC TACATCTGGT ACCTTGGCTG GCATTATGGG AATGAGGTTT 240  
TACCACTCTG GAAAATTCAT GCCTGCAGGT TTAATTGCAG GTGCCAGTTT GCTGATGGTC 300  
GCCAAAGTTG GAGTTAGTAT GTTCAACAGA CCCCAT 336

Sequence No.: 40  
Sequence length: 342  
Sequence type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Sequence kind: cDNA to mRNA  
Original source:  
Organism species: *Homo sapiens*  
Cell kind: Epidermoid carcinoma  
Cell line: KB  
Clone name: HP10179  
Sequence description

ATGGAGAAGC CCCTCTTCCC ATTAGTGCC T TGCAATTGGT TTGGCTTTGG CTACACAGCA 60  
CTGTTTGT TT CTGGTGGGAT CGTTGGCTAT GTAAAAACAG GCAGCGTGCC GTCCCTGGCT 120  
GCAGGGCTGC TCTTCGGCAG TCTAGCCGGC CTGGGTGCTT ACCAGCTGTA TCAGGATCCA 180  
AGGAACGTTT GGGGTTTCTT AGCCGCTACA TCTGTACTT TTGTTGGTGT TATGGGAATG 240  
AGATCCTACT ACTATGAAA ATTCATGCCT GTAGGTTTAA TTGCAGGTGC CAGTTTGCTG 300  
ATGGCCGCCA AAGTTGGAGT TCGTATGTTG ATGACATCTG AT 342

Sequence No.: 41  
Sequence length: 981  
Sequence type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Sequence kind: cDNA to mRNA  
Original source:  
Organism species: *Homo sapiens*  
Cell kind: Fibrosarcoma  
Cell line: HT-1080  
Clone name: HP10196  
Sequence description

ATGGCGGCGG	CGGCGGCGGC	GGCTGCAGCT	ACGAACGGGA	CCGGAGGAAG	CAGCGGGATG	60
GAGGTGGATG	CAGCAGTAGT	CCCCAGCGTG	ATGGCCTGCG	GAGTGA CTGG	GAGTGTTTCC	120
GTCGCTCTCC	ATCCCCTTGT	CATTCTCAAC	ATCTCAGACC	ACTGGATCCG	CATGCGCTCC	180
CAGGAGGGGC	GGCCTGTGCA	GGTGATTGGG	GCTCTGATTG	GCAAGCAGGA	GGGCCGAAAT	240
ATCGAGGTGA	TGAATCCTT	TGAGCTGCTG	TCCCACACCG	TGGAAGAGAA	GATTATCATT	300
GACAAGGAAT	ATTATTACAC	CAAGGAGGAG	CAGTTTAAAC	AGGTGTTCAA	GGAGCTGGAG	360
TTTCTGGGTT	GGTATACCAC	AGGGGGGCCA	CCTGACCCCT	CGGACATCCA	CGTCCATAAG	420
CAGGTGTGTG	AGATCATCGA	GAGCCCCCTC	TTTCTGAAGT	TGAACCCTAT	GACCAAGCAC	480
ACAGATCTTC	CTGTCAAGCT	TTTTGAGTCT	GTCAATGATA	TAATCAATGG	AGAGGCCACA	540
ATGCTGTTTG	CTGAGCTGAC	CTACACTCTG	GCCACAGAGG	AAGCGGAACG	CATTGGTGTA	600
GACCACGTAG	CCCGAATGAC	AGCAACAGGC	AGTGGAGAGA	ACTCCACTGT	GGCTGAACAC	660
CTGATAGCAC	AGCACAGCGC	CATCAAGATG	CTGCACAGCC	GCGTCAAGCT	CATCTTGGAG	720
TACGTCAAGG	CCTCTGAAGC	GGGAGAGGTC	CCCTTTAATC	ATGAGATCCT	GCGGGAGGCC	780
TATGCTCTGT	GTCAGTGTCT	CCCGGTGCTC	AGCACAGACA	AGTTCAAGAC	AGATTTTAT	840
GATCAATGCA	ACGACGTGGG	GCTCATGGCC	TACCTCGGCA	CCATCACCAA	AACGTGCAAC	900
ACCATGAACC	AGTTTGTGAA	CAAGTTCAAT	GTCTCTACG	ACCGACAAGG	CATCGGCAGG	960
AGAATGCGCG	GGCTCTTTTT	C				981

Sequence No.: 42  
Sequence length: 1119  
Sequence type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Sequence kind: cDNA to mRNA  
Original source:  
Organism species: *Homo sapiens*  
Cell kind: Fibrosarcoma  
Cell line: HT-1080  
Clone name: HP10235  
Sequence description

ATGACCCTAT	GTGCCATGCT	CCCCCTGCTG	TTATTCACCT	ACCTCAACTC	CTTCCTGCAT	60
CAGAGGATCC	CCCAGTCCGT	ACGGATCCTG	GGCAGCCTGG	TGGCCATCCT	GCTGGTGTTT	120
CTGATCACTG	CCATCCTGGT	GAAGGTGCAG	CTGGATGCTC	TGCCCTTCTT	TGTCATCACC	180
ATGATCAAGA	TCGTGCTCAT	TAATTCATTT	GGTGCCATCC	TGCAGGGCAG	CCTGTTTGTT	240
CTGGCTGGCC	TTCTGCCTGC	CAGCTACACG	GGCCCCATCA	TGAGTGCCCA	GGGCCTAGCA	300
GGCTTCTTTG	CCTCCGTGGC	CATGATCTGC	GCTATTGCCA	GTGGCTCGGA	GCTATCAGAA	360
AGTGCCTTCG	GCTACTTTAT	CACAGCCTGT	GCTGTTATCA	TTTTGACCAT	CATCTGTTAC	420
CTGGGCCTGC	CCCGCCTGGA	ATTCTACCGC	TACTACCAGC	AGCTCAAGCT	TGAAGGACCC	480
GGGGAGCAGG	AGACCAAGTT	GGACCTCATT	AGCAAAGGAG	AGGAGCCAAG	AGCAGGCAAA	540
GAGGAATCTG	GAGTTTCAGT	CTCCAACCTC	CAGCCCACCA	ATGAAAGCCA	CTCTATCAAA	600
GCCATCCTGA	AAAATATCTC	AGTCCTGGCT	TTCTCTGTCT	GCTTCATCTT	CACTATCACC	660
ATTGGGATGT	TTCCAGCCGT	GACTGTTGAG	GTCAAGTCCA	GCATCGCAGG	CAGCAGCACC	720
TGGGAACGTT	ACTTCATTCC	TGTGTCCTGT	TTCTTGACTT	TCAATATCTT	TGACTGGTTG	780
GGCCGGAGCC	TCACAGCTGT	ATTGATGTGG	CCTGGGAAGG	ACAGCCGCTG	GCTGCCAAGC	840
CTGGTGCTGG	CCCGGCTGGT	GTTTGTGCCA	CTGCTGCTGC	TGTGCAACAT	TAAGCCCCGC	900
CGCTACCTGA	CTGTGGTCTT	CGAGCACGAT	GCCTGGTTCA	TCTTCTTCAT	GGCTGCCTTT	960
GCCTTCTCCA	ACGGCTACCT	CGCCAGCCTC	TGCATGTGCT	TCGGGCCCCA	GAAAGTGAAG	1020
CCAGCTGAGG	CAGAGACCGC	AGGAGCCATC	ATGGCCTTCT	TCCTGTGTCT	GGGTCTGGCA	1080
CTGGGGGCTG	TTTTCTCCTT	CCTGTTCCGG	GCAATTGTG			1119

Sequence No.: 43

Sequence length: 549

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10297

Sequence description

ATGAAGCTCT	TATCTTTGGT	GGCTGTGGTC	GGGTGTTTGC	TGGTGCCCCC	AGCTGAAGCC	60
AACAAGAGTT	CTGAAGATAT	CCGGTGCAAA	TGCATCTGTC	CACCTTATAG	AAACATCAGT	120
GGGCACATTT	ACAACCAGAA	TGTATCCCAG	AAGGACTGCA	ACTGCCTGCA	CGTGGTGGAG	180
CCCATGCCAG	TGCCTGGCCA	TGACGTGGAG	GCCTACTGCC	TGCTGTGCGA	GTGCAGGTAC	240
GAGGAGCGCA	GCACCACCAC	CATCAAGGTC	ATCATTGTCA	TCTACCTGTC	CGTGGTGGGT	300
GCCCTGTTGC	TCTACATGGC	CTTCCTGATG	CTGGTGGACC	CTCTGATCCG	AAAGCCGGAT	360
GCATACACTG	AGCAACTGCA	CAATGAGGAG	GAGAATGAGG	ATGCTCGCTC	TATGGCAGCA	420
GCTGCTGCAT	CCCTCGGGGG	ACCCCGAGCA	AACACAGTCC	TGGAGCGTGT	GGAAGGTGCC	480
CAGCAGCGGT	GGAAGCTGCA	GGTGCAGGAG	CAGCGGAAGA	CAGTCTTCGA	TCGGCACAAG	540
ATGCTCAGC						549

Sequence No.: 44

Sequence length: 348

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10299

Sequence description

ATGGCCAGTA	CAGTGGTAGC	AGTTGGACTG	ACCATTGCTG	CTGCAGGATT	TGCAGGCCGT	60
TACGTTTTGC	AAGCCATGAA	GCATATGGAG	CCTCAAGTAA	AACAAGTTTT	TCAAAGCCTA	120
CCAAAATCTG	CCTTCAGTGG	TGGCTATTAT	AGAGGTGGGT	TTGAACCCAA	AATGACAAAA	180
CGGGAAGCA	GCATTAATAC	TAGGTGTAAG	CCCTACTGCC	AATAAAGGGA	AAATAAGAGA	240
GCTCATCGAC	GAATTATGCT	TTTAAATCAT	CCTGACAAAG	GAGGATCTCC	TTATATAGCA	300
GCCAAAATCA	ATGAAGCTAA	AGATTTACTA	GAAGGTCAAG	CTAAAAAA		348

Sequence No.: 45

Sequence length: 456

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10301

Sequence description

ATGGCTGTCC	TCTCTAAGGA	ATATGGTTTT	GTGCTTCTAA	CTGGTGCTGC	CAGCTTTATA	60
ATGGTGGCCC	ACCTAGCCAT	CAATGTTTCC	AAGGCCCGCA	AGAAGTACAA	AGTGGAGTAT	120
CCTATCATGT	ACAGCACGGA	CCCTGAAAAT	GGGCACATCT	TCAACTGCAT	TCAGCGAGCC	180
CACCAGAACA	CGTTGGAAGT	GTATCCTCCC	TTCTTATTTT	TTCTAGCTGT	TGGAGGTGTT	240
TACCACCCGC	GTATAGCTTC	TGGCCTGGGC	TTGGCCTGGA	TTGTTGGACG	AGTTCTTTAT	300
GCTTATGGCT	ATTACACGGG	AGAACCCAGC	AAGCGTAGTC	GAGGAGCCCT	GGGGTCCATC	360
GCCCTCCTGG	GCTTGGTGGG	CACAACTGTG	TGCTCTGCTT	TCCAGCATCT	TGGTTGGGTT	420
AAAAGTGGCT	TGGGCAGTGG	ACCCAAATGC	TGCCAT			456

Sequence No.: 46  
Sequence length: 1677  
Sequence type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Sequence kind: cDNA to mRNA  
Original source:  
Organism species: *Homo sapiens*  
Cell kind: Liver  
Clone name: HP10302  
Sequence description

ATGGCCCCCA	CGCTGCAACA	GGCGTACCGG	AGGCGCTGGT	GGATGGCCTG	CACGGCTGTG	60
CTGGAGAACC	TCTTCTTCTC	TGCTGTACTC	CTGGGCTGGG	GCTCCCTGTT	GATCATTCTG	120
AAGAACGAGG	GCTTCTATTG	CAGCACGTGC	CCAGCTGAGA	GCAGCACCAA	CACCACCCAG	180
GATGAGCAGC	GCAGGTGGCC	AGGCTGTGAC	CAGCAGGACG	AGATGCTCAA	CCTGGGCTTC	240
ACCATTGGTT	CCTTCGTGCT	CAGCGCCACC	ACCTTGCCAC	TGGGGATCCT	CATGGACCGC	300
TTTGGCCCCC	GACCCGTGCG	GCTGGTTGGC	AGTGCCTGCT	TCACTGCGTC	CTGCACCCCTC	360
ATGGCCCTGG	CCTCCCGGGA	CGTGGAAGCT	CTGTCTCCGT	TGATATTCCT	GGCGCTGTCC	420
CTGAATGGCT	TTGGTGGCAT	CTGCCTAAGC	TTCACCTCAC	TCACGCTGCC	CAACATGTTT	480
GGGAACCTGC	GCTCCACGTT	AATGGCCCTC	ATGATTGGCT	CTTACGCCTC	TTCTGCCATT	540
ACGTTCCAG	GAATCAAGCT	GATCTACGAT	GCCGGTGTGG	CCTTCGTGGT	CATCATGTTC	600
ACCTGGTCTG	GCCTGGCCTG	CCTTATCTTT	CTGAACTGCA	CCCTCAACTG	GCCCATCGAA	660
GCCTTTCCTG	CCCCTGAGGA	AGTCAATTAC	ACGAAGAAGA	TCAAGCTGAG	TGGGCTGGCC	720
CTGGACCACA	AGGTGACAGG	TGACCTCTTC	TACACCCATG	TGACCACCAT	GGGCCAGAGG	780
CTCAGCCAGA	AGGCCCCAG	CCTGGAGGAC	GGTTCGGATG	CCTTCATGTC	ACCCCAGGAT	840
GTTCGGGGCA	CCTCAGAAAA	CCTTCCTGAG	AGGTCTGTCC	CCTTACGCAA	GAGCCTCTGC	900
TCCCCCACTT	TCCTGTGGAG	CCTCCTCACC	ATGGGCATGA	CCCAGCTGCG	GATCATCTTC	960
TACATGGCTG	CTGTGAACAA	GATGCTGGAG	TACCTTGTGA	CTGGTGGCCA	GGAGCATGAG	1020
ACAAATGAAC	AGCAACAAAA	GGTGGCAGAG	ACAGTTGGGT	TCTACTCCTC	CGTCTTCGGG	1080
GCCATGCAGC	TGTTGTGCCT	TCTCACCTGC	CCCCTCATTG	GCTACATCAT	GGACTGGCGG	1140
ATCAAGGACT	GCGTGGACGC	CCCAACTCAG	GGCACTGTCC	TCGGAGATGC	CAGGGACGGG	1200
GTTGCTACCA	AATCCATCAG	ACCACGCTAC	TGCAAGATCC	AAAAGCTCAC	CAATGCCATC	1260
AGTGCCTTCA	CCCTGACCAA	CCTGCTGCTT	GTGGGTTTTG	GCATCACCTG	TCTCATCAAC	1320
AACTTACACC	TCCAGTTTGT	GACCTTTGTC	CTGCACACCA	TTGTTGAGG	TTTCTTCCAC	1380
TCAGCCTGTG	GGAGTCTCTA	TGCTGCAGTG	TTCCCATCCA	ACCACTTTGG	GACGCTGACA	1440
GGCCTGCAGT	CCCTCATCAG	TGCTGTGTTT	GCCTTGCTTC	AGCAGCCACT	TTTCATGGCG	1500
ATGGTGGGAC	CCCTGAAAGG	AGAGCCCTTC	TGGGTGAATC	TGGGCCTCCT	GCTATTCTCA	1560
CTCCTGGGAT	TCCTGTTGCC	TTCTTACCTC	TTCTATTACC	GTGCCCGGCT	CCAGCAGGAG	1620
TACGCCGCCA	ATGGGATGGG	CCCACTGAAG	GTGCTTAGCG	GCTCTGAGGT	GACCGCA	1677

Sequence No.: 47  
Sequence length: 990

WO 98/21328

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Sequence type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Sequence kind: cDNA to mRNA  
Original source:  
Organism species: *Homo sapiens*  
Cell kind: Osteosarcoma  
Cell line: U-2 OS  
Clone name: HP10304  
Sequence description

ATGGAGGGCG CTCCACCGGG GTCGCTCGCC CTCCGGCTCC TGCTGTTTCT GCGCTACCC 60  
GCCTCCGGCT GGCTGACGAC GGGCGCCCCC GAGCCGCCCG CGCTGTCCGG AGCCCCACAG 120  
GACGGCATCA GAATTAATGT AACTACACTG AAAGATGATG GGGACATATC TAAACAGCAG 180  
GTTGTTCTTA ACATAACCTA TGAGAGTGGA CAGGTGTATG TAAATGACTT ACCTGTAAAT 240  
AGTGGTGTA CCCGAATAAG CTGTCAGACT TTGATAGTGA AGAATGAAAA TCTTGAAAAAT 300  
TTGGAGGAAA AAGAATATTT TGAATTGTC AGTGTAAGGA TTTTAGTTCA TGAGTGGCCT 360  
ATGACATCTG GTTCCAGTTT GCAACTAATT GTCATTCAAG AAGAGGTAGT AGAGATTGAT 420  
GGAAAAAAG TTCAGCAAAA GGATGTCACT GAAATTGATA TTTTAGTTAA GAACCGGGGA 480  
GTACTCAGAC ATTCAAATA TACCCTCCCT TTGGAAGAAA GCATGCTCTA CTCTATTTCT 540  
CGAGACAGTG ACATTTTATT TACCCTTCCT AACCTCTCCA AAAAAGAAAAG TGTTAGTTCA 600  
CTGCAAAACCA CTAGCCAGTA TCTTATCAGG AATGTGGAAG CCACTGTAGA TGAAGATGTT 660  
TTACCTGGCA AGTTACCTGA AACTCCTCTC AGAGCAGAGC CGCCATCTTC ATATAAGGTA 720  
ATGTGTCAGT GGATGGAAAA GTTTAGAAAA GATCTGTGTA GGTTCCTGGAG CAACGTTTTC 780  
CCAGTATTCT TTCAGTTTTT GAACATCATG GTGGTTGGAA TTACAGGAGC AGCTGTGGTA 840  
ATAACCATCT TAAAGGTGTT TTTCCAGTT TCTGAATACA AAGGAATTCT TCAGTTGGAT 900  
AAAGTGGACG TCATACCTGT GACAGCTATC AACTTATATC CAGATGGTCC AGAGAAAAGA 960  
GCTGAAAACC TTGAAGATAA AACATGTATT 990

Sequence No.: 48  
Sequence length: 324  
Sequence type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Sequence kind: cDNA to mRNA  
Original source:  
Organism species: *Homo sapiens*  
Cell kind: Osteosarcoma  
Cell line: U-2 OS  
Clone name: HP10305  
Sequence description

ATGAGTCTGA CTTCCAGTTC CAGCGTACGA GTTGAATGGA TCGCAGCAGT TACCATTGCT 60



132

GCTGGGACAG CTGCAATTGG TTATCTAGCT TACAAAAGAT TTTATGTTAA AGATCATCGA 120  
AATAAAGCTA TGATAAACCT TCACATCCAG AAAGACAACC CCAAGATAGT ACATGCTTTT 180  
GACATGGAGG ATTTGGGAGA TAAAGCTGTG TACTGCCGTT GTTGGAGGTC CAAAAAGTTC 240  
CCATTCTGTG ATGGGGCTCA CACAAAACAT AACGAAGAGA CTGGAGACAA TGTGGGCCCT 300  
CTGATCATCA AGAAAAAAGA AACT 324

Sequence No.: 49

Sequence length: 303

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Oosterosarcoma

Cell line: U-2 OS

Clone name: HP10306

Sequence description

ATGAACCTGG AGCGAGTGTG CAATGAGGAG AAATTGAACC TGTGCCGGAA GTACTACCTG 60  
GGGGGGTTTG CTTTCCTGCC TTTTCTCTGG TTGGTCAACA TCTTCTGGTT CTTCCGAGAG 120  
GCCTTCCTTG TCCAGCCTA CACAGAACAG AGCCAAATCA AAGGCTATGT CTGGCGCTCA 180  
GCTGTGGGCT TCCTCTTCTG GGTGATAGTG CTCACCTCCT GGATCACCAT CTTCCAGATC 240  
TACCGGCCCC GCTGGGGTGC CCTTGGGGAC TACCTCTCCT TCACCATACC CCTGGGCACC 300  
CCC 303

Sequence No.: 50

Sequence length: 1116

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10328

Sequence description

ATGAAGTATC TCCGGCACCG GCGGCCCAAT GCCACCCTCA TTCTGGCCAT CGGCGCTTTC 60  
ACCCTCCTCC TCTTCAGTCT GCTAGTGTCA CCACCCACCT GCAAGGTCCA GGAGCAGCCA 120  
CCGGCGATCC CCGAGGCCCT GGCCTGGCCC ACTCCACCCA CCCGCCCAGC CCCGGCCCCG 180

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TGCCATGCCA ACACCTCTAT GGTCACCCAC CCGGACTTCG CCACGCAGCC GCAGCACGTT 240
CAGAACTTCC TCCTGTACAG AACTGCCGC CACTTTCCCC TGCTGCAGGA CGTGCCCCCC 300
TCTAAGTCCG CGCAGCCGGT CTTCTGCTG CTGGTGATCA AGTCCTCCCC TAGCAACTAT 360
GTGCGCCGCG AGCTGCTGCG GCGCACGTGG GGCCGCGAGC GCAAGGTACG GGGTTTGCAG 420
CTGCGCCTCC TCTTCTGGT GGGCACAGCC TCCAACCCGC ACGAGGCCCG CAAGGTCAAC 480
CGGCTGCTGG AGCTGGAGGC ACAGACTCAC GGAGACATCC TGCAGTGGGA CTTCCACGAC 540
TCCTTCTTCA ACCTCACGCT CAAGCAGGTC CTGTTCTTAC AGTGGCAGGA GACAAGGTGC 600
GCCAACGCCA GCTTCGTGCT CAACGGGGAT GATGACGTCT TTGCACACAC AGACAACATG 660
GTCTTCTACC TGCAGGACCA TGACCCTGGC CGCCACCTCT TCGTGGGGCA ACTGATCCAA 720
AACGTGGGCC CCATCCGGGC TTTTGGAGC AAGTACTATG TGCCAGAGGT GGTGACTCAG 780
AATGAGCGGT ACCCACCCTA TTGTGGGGGT GGTGGCTTCT TGCTGTCCCG CTTACGGGCC 840
GCTGCCCTGC GCCGTGCTGC CCATGTCTTG GACATCTTCC CCATTGATGA TGTCTTCCTG 900
GGTATGTGTC TGGAGCTTGA GGGACTGAAG CCTGCCTCCC ACAGCGGCAT CCGCACGTCT 960
GGCGTGCGGG CTCCATCGCA ACACCTGTCC TCCTTTGACC CCTGCTTCTA CCGAGACCTG 1020
CTGCTGGTGC ACCGCTTCTT ACCTTATGAG ATGCTGCTCA TGTGGGATGC GCTGAACCAG 1080
CCCAACCTCA CCTGCGGCAA TCAGACACAG ATCTAC 1116

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Sequence No.: 51

Sequence length: 986

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP00442

Sequence characteristics

Code representing characteristics: CDS

Existence site: 82.. 699

Characterization method: E

Sequence description

```

AGACTGCGGG ACGGACGGTG GACGCTGGGA CGCGTTTGTA GCTCCGGCCC CGCCGTTCCG 60
ACCCCCGCCG CCGTCGCCGC C ATG ACG GGG CTA GCA CTG CTC TAC TCC GGG 111
Met Thr Gly Leu Ala Leu Leu Tyr Ser Gly
1 5 10
GTC TTC GTG GCC TTC TGG GCC TGC GCG CTG GCC GTG GGA GTC TGC TAC 159
Val Phe Val Ala Phe Trp Ala Cys Ala Leu Ala Val Gly Val Cys Tyr
15 20 25
ACC ATT TTT GAT TTG GGC TTC CGC TTT GAT GTG GCA TGG TTC CTG ACG 207
Thr Ile Phe Asp Leu Gly Phe Arg Phe Asp Val Ala Trp Phe Leu Thr

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134

30	35	40	
GAG ACT TCG CCC TTC ATG TGG TCC AAC CTG GGC ATT GGC CTA GCT ATC			255
Glu Thr Ser Pro Phe Met Trp Ser Asn Leu Gly Ile Gly Leu Ala Ile			
45	50	55	
TCC CTG TCT GTG GTT GGG GCA GCC TGG GGC ATC TAT ATT ACC GGC TCC			303
Ser Leu Ser Val Val Gly Ala Ala Trp Gly Ile Tyr Ile Thr Gly Ser			
60	65	70	
TCC ATC ATT GGT GGA GGA GTG AAG GCC CCC AGG ATC AAG ACC AAG AAC			351
Ser Ile Ile Gly Gly Gly Val Lys Ala Pro Arg Ile Lys Thr Lys Asn			
75	80	85	90
CTG GTC AGC ATC ATC TTC TGT GAG GCT GTG GCC ATC TAC GGC ATC ATC			399
Leu Val Ser Ile Ile Phe Cys Glu Ala Val Ala Ile Tyr Gly Ile Ile			
95	100	105	
ATG GCA ATT GTC ATT AGC AAC ATG GCT GAG CCT TTC AGT GCC ACA GAC			447
Met Ala Ile Val Ile Ser Asn Met Ala Glu Pro Phe Ser Ala Thr Asp			
110	115	120	
CCC AAG GCC ATC GGC CAT CGG AAC TAC CAT GCA GGC TAC TCC ATG TTT			495
Pro Lys Ala Ile Gly His Arg Asn Tyr His Ala Gly Tyr Ser Met Phe			
125	130	135	
GGG GCT GGC CTC ACC GTA GGC CTG TCT AAC CTC TTC TGT GGA GTC TGC			543
Gly Ala Gly Leu Thr Val Gly Leu Ser Asn Leu Phe Cys Gly Val Cys			
140	145	150	
GTG GGC ATC GTG GGC AGT GGG GCT GCC CTG GCC GAT GCT CAG AAC CCC			591
Val Gly Ile Val Gly Ser Gly Ala Ala Leu Ala Asp Ala Gln Asn Pro			
155	160	165	170
AGC CTC TTT GTA AAG ATT CTC ATC GTG GAG ATC TTT GGC AGC GCC ATT			639
Ser Leu Phe Val Lys Ile Leu Ile Val Glu Ile Phe Gly Ser Ala Ile			
175	180	185	
GGC CTC TTT GGG GTC ATC GTC GCA ATT CTT CAG ACC TCC AGA GTG AAG			687
Gly Leu Phe Gly Val Ile Val Ala Ile Leu Gln Thr Ser Arg Val Lys			
190	195	200	
ATG GGT GAC TAGATGATAT GTGTGGGTGG GGCCGTGCCT CACT			730
Met Gly Asp			
205			
TTTATTTTATT GCTGGTTTTTC CTGGGACAGC TGGAGCTGTG TCCCTTAGCC TTTCAGAGGC			790
TTGGTGTTCA GGGCCCTCCC TGCACTCCCC TCTTGCTGCG TGTTGATTG GAGGCACTGC			850
AGTCCAGGCC GAGTCCTCAG TCGGGGAGC AGGCTGCTGC TGCTGACTCT GTGCAGCTGC			910
GCACCTGTGT CCCCCACCTC CACCCTCAAC CCATCTTCCT AGTGTTTGTG AAATAAACTT			970
GGTATTTGTC TGGGTC			986

Sequence No.: 52

Sequence length: 1824

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Leukocyte

Clone name: HP00804

Sequence characteristics

Code representing characteristics: CDS

Existence site: 133.. 1248

Characterization method: E

Sequence description

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GGCCCAGCTG AGCGGCCGCC GAGCGGGTGC GGGTGCAGGC GCATCGGCCA TCACCGCGCG 60
GCCGCGCAGC GGACACCGTG CGTACCGGCC TCGGCGCCCC GGCCACCGGG GCGGACCGCG 120
GAACCCGAGG CC ATG TCC CAT GAA AAG AGT TTT TTG GTG TCT GGG GAC AAC 171
      Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn
          1             5             10
TAT CCT CCC CCC AAC CCT GGA TAT CCG GGG GGG CCC CAG CCA CCC ATG 219
Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met
      15             20             25
CCC CCC TAT GCT CAG CCT CCC TAC CCT GGG GCC CCT TAC CCA CAG CCC 267
Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro
      30             35             40             45
CCT TTC CAG CCC TCC CCC TAC GGT CAG CCA GGG TAC CCC CAT GGC CCC 315
Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro
          50             55             60
AGC CCC TAC CCC CAA GGG GGC TAC CCA CAG GGT CCC TAC CCC CAA GGG 363
Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly
      65             70             75
GGC TAC CCA CAG GGC CCC TAC CCA CAA GAG GGC TAC CCA CAG GGC CCC 411
Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro
      80             85             90
TAC CCC CAA GGG GGC TAC CCC CAG GGG CCA TAT CCC CAG AGC CCC TTC 459
Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe
      95             100             105
CCC CCC AAC CCC TAT GGA CAG CCA CAG GTC TTC CCA GGA CAA GAC CCT 507
Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro
      110             115             120             125
GAC TCA CCC CAG CAT GGA AAC TAC CAG GAG GAG GGT CCC CCA TCC TAC 555
Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr
          130             135             140
TAT GAC AAC CAG GAC TTC CCT GCC ACC AAC TGG GAT GAC AAG AGC ATC 603
Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile

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145	150	155	651
CGA CAG GCC TTC ATC CGC AAG GTG TTC CTA GTG CTG ACC TTG CAG CTG			
Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu			
160	165	170	699
TCG GTG ACC CTG TCC ACG GTG TCT GTG TTC ACT TTT GTT GCG GAG GTG			
Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val			
175	180	185	747
AAG GGC TTT GTC CGG GAG AAT GTC TGG ACC TAC TAT GTC TCC TAT GCT			
Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala			
190	195	200	795
GTC TTC TTC ATC TCT CTC ATC GTC CTC AGC TGT TGT GGG GAC TTC CGG			
Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg			
210	215	220	843
CGA AAG CAC CCC TGG AAC CTT GTT GCA CTG TCG GTC CTG ACC GCC AGC			
Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser			
225	230	235	891
CTG TCG TAC ATG GTG GGG ATG ATC GCC AGC TTC TAC AAC ACC GAG GCA			
Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala			
240	245	250	939
GTC ATC ATG GCC GTG GGC ATC ACC ACA GCC GTC TGC TTC ACC GTC GTC			
Val Ile Met Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val			
255	260	265	987
ATC TTC TCC ATG CAG ACC CGC TAC GAC TTC ACC TCA TGC ATG GGC GTG			
Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val			
270	275	280	1035
CTC CTG GTG AGC ATG GTG GTG CTC TTC ATC TTC GCC ATT CTC TGC ATC			
Leu Leu Val Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile			
290	295	300	1083
TTC ATC CGG AAC CGC ATC CTG GAG ATC GTG TAC GCC TCA CTG GGC GCT			
Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala			
305	310	315	1131
CTG CTC TTC ACC TGC TTC CTC GCA GTG GAC ACC CAG CTG CTG CTG GGC			
Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly			
320	325	330	1179
AAC AAG CAG CTG TCC CTG AGC CCA GAA GAG TAT GTG TTT GCT GCG CTG			
Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu			
335	340	345	1227
AAC CTG TAC ACA GAC ATC ATC AAC ATC TTC CTG TAC ATC CTC ACC ATC			
Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile			
350	355	360	1270
ATT GGC CGC GCC AAG GAG TAGCCGAGCT CCAGCTCGCT GTGCC			
Ile Gly Arg Ala Lys Glu			
370			1330
CGCTCAGGTG GCACGGCTGG CCTGGACCCT GCCCCTGGCA CGGCAGTGCC AGCTGTACTT			

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CCCCCTCTCTC TTGTCCCCAG GCACAGCCTA GGGAAAAGGA TGCCTCTCTC CAACCCCTCCT 1390
GTATGTACAC TGCAGATACT TCCATTTGGA CCCGCTGTGG CCACAGCATG GCCCCTTTAG 1450
TCCTCCCGCC CCCGCCAAGG GGCACCAAGG CCACGTTTCC GTGCCACCTC CTGTCTACTC 1510
ATTGTTGCAT GAGCCCTGTC TGCCAGCCCA CCCAGGGAC TGGGGGCAGC ACCAGGTCCC 1570
GGGGAGAGGG ATTGAGCCAA GAGGTGAGGG TGCACGTCTT CCCTCCTGTC CCAGCTCCCC 1630
AGCCTGGCGT AGAGCACCCC TCCCCTCCCC CCCACCCCCC TGGAGTGCTG CCCTCTGGGG 1690
ACATGCGGAG TGGGGGTCTT ATCCCTGTGC TGAGCCCTGA GGGCAGAGAG GATGGCATGT 1750
TTCAGGGGAG GGGGAAGCCT TCCTCTCAAT TTGTTGTCAG TGAAATTCCA ATAAATGGGA 1810
TTTGCTCTCT GCCT 1824

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Sequence No.: 53

Sequence length: 1076

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP01098

Sequence characteristics

Code representing characteristics: CDS

Existence site: 62.. 601

Characterization method: E

Sequence description

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AGTTCCGCCC GCTGGTCATC GCGCCCTTTC CCCTGCCGGT GTCCTGCTCG CCGTCCCCGC 60
C ATG CTG TCT CTA GAC TTT TTG GAC GAT GTG CCG CGG ATG AAC AAG CGG 109
Met Leu Ser Leu Asp Phe Leu Asp Asp Val Arg Arg Met Asn Lys Arg
1 5 10 15
CAG CTC TAT TAT CAA GTC CTA AAT TTT GGA ATG ATT GTC TCA TCG GCA 157
Gln Leu Tyr Tyr Gln Val Leu Asn Phe Gly Met Ile Val Ser Ser Ala
20 25 30
CTA ATG ATC TGG AAG GGG TTA ATG GTA ATA ACT GGA AGT GAA AGT CCG 205
Leu Met Ile Trp Lys Gly Leu Met Val Ile Thr Gly Ser Glu Ser Pro
35 40 45
ATT GTA GTG GTG CTC AGT GGC AGC ATG GAA CCT GCA TTT CAT AGA GGA 253
Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala Phe His Arg Gly
50 55 60
GAT CTT CTC TTT CTA ACA AAT CGA GTT GAA GAT CCC ATA CGA GTG GGA 301
Asp Leu Leu Phe Leu Thr Asn Arg Val Glu Asp Pro Ile Arg Val Gly
65 70 75 80
GAA ATT GTT GTT TTT AGG ATA GAA GGA AGA GAG ATT CCT ATA GTT CAC 349

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Glu Ile Val Val Phe Arg Ile Glu Gly Arg Glu Ile Pro Ile Val His  
 85 90 95 397  
 CGA GTC TTG AAG ATT CAT GAA AAG CAA AAT GGG CAT ATC AAG TTT TTG  
 Arg Val Leu Lys Ile His Glu Lys Gln Asn Gly His Ile Lys Phe Leu  
 100 105 110 445  
 ACC AAA GGA GAT AAT AAT GCG GTT GAT GAC CGA GGC CTC TAT AAA CAA  
 Thr Lys Gly Asp Asn Asn Ala Val Asp Asp Arg Gly Leu Tyr Lys Gln  
 115 120 125 493  
 GGA CAA CAT TGG CTA GAG AAA AAA GAT GTT GTG GGG AGA GCC AGG GGA  
 Gly Gln His Trp Leu Glu Lys Lys Asp Val Val Gly Arg Ala Arg Gly  
 130 135 140 541  
 TTT GTT CCT TAT ATT GGA ATT GTG ACG ATC CTC ATG AAT GAC TAT CCT  
 Phe Val Pro Tyr Ile Gly Ile Val Thr Ile Leu Met Asn Asp Tyr Pro  
 145 150 155 160 589  
 AAA TTT AAG TAT GCA GTT CTC TTT TTG CTG GGT TTA TTC GTG CTG GTT  
 Lys Phe Lys Tyr Ala Val Leu Phe Leu Leu Gly Leu Phe Val Leu Val  
 165 170 175 630  
 CAT CGT GAG TA AGAAGCC TGCCTTGCTG TTCCTGGGAA GAT  
 His Arg Glu  
 GCCATAGTTT TCGTTACTGG ATGTTTGGAG TAGATACTGG TCTGTGATTG GTGGAATGGA 690  
 GAACACACGT GTTGGTGCTT CTGGGTAGCA CTGGTTTGCA TTAGTTTATG TTTCCATGCC 750  
 AGAGTTTGTG TGGGCGGGCG CATGTGCACC ACAGAGTGCA CTCGAGGGGA CTTTCAGTCA 810  
 CAGGATTTC AATTGTTCAT TGTCACACTT TCAAATTTTT GTACATCAGT GAATTTTTTT 870  
 ATATTA AAAAG GTTGAGCCAA AGCCCCCAGT GTTTGTATTT TGAAGCCAAG CTTCACTTCT 930  
 AAAGTGCCTA CAGAGACTTG TAAATGAAAA TGCAGCTCTG CACGAGTTTG AAACCGTCAT 990  
 ACCTCCTTCT ATTAGGAATG GCATATACTG AGGTGGTCGT AAGTCTTAAC TTCTAAAATT 1050  
 TTAAATAAAA GACTTTGCAC ATTGAG 1076

Sequence No.: 54

Sequence length: 1591

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01148

Sequence characteristics

Code representing characteristics: CDS

Existence site: 102.. 1145

Characterization method: E

## Sequence description

GTCCCTCCTC TTAACATACT TGCAGCTAAA ACTAAATATT GCTGCTTGGG GACCTCCTTC 60  
 TAGCCTTAAA TTTCAGCTCA TCACCTTCAC CTGCCTTGGT C ATG GCT CTG CTA TTC 116  
 Met Ala Leu Leu Phe  
 1 5  
 TCC TTG ATC CTT GCC ATT TGC ACC AGA CCT GGA TTC CTA GCG TCT CCA 164  
 Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly Phe Leu Ala Ser Pro  
 10 15 20  
 TCT GGA GTG CGG CTG GTG GGG GGC CTC CAC CGC TGT GAA GGG CGG GTG 212  
 Ser Gly Val Arg Leu Val Gly Gly Leu His Arg Cys Glu Gly Arg Val  
 25 30 35  
 GAG GTG GAA CAG AAA GGC CAG TGG GGC ACC GTG TGT GAT GAC GGC TGG 260  
 Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val Cys Asp Asp Gly Trp  
 40 45 50  
 GAC ATT AAG GAC GTG GCT GTG TTG TGC CGG GAG CTG GGC TGT GGA GCT 308  
 Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu Leu Gly Cys Gly Ala  
 55 60 65  
 GCC AGC GGA ACC CCT AGT GGT ATT TTG TAT GAG CCA CCA GCA GAA AAA 356  
 Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu Pro Pro Ala Glu Lys  
 70 75 80 85  
 GAG CAA AAG GTC CTC ATC CAA TCA GTC AGT TGC ACA GGA ACA GAA GAT 404  
 Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys Thr Gly Thr Glu Asp  
 90 95 100  
 ACA TTG GCT CAG TGT GAG CAA GAA GAA GTT TAT GAT TGT TCA CAT GAA 452  
 Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr Asp Cys Ser His Glu  
 105 110 115  
 GAA GAT GCT GGG GCA TCG TGT GAG AAC CCA GAG AGC TCT TTC TCC CCA 500  
 Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu Ser Ser Phe Ser Pro  
 120 125 130  
 GTC CCA GAG GGT GTC AGG CTG GCT GAC GGC CCT GGG CAT TGC AAG GGA 548  
 Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro Gly His Cys Lys Gly  
 135 140 145  
 CGC GTG GAA GTG AAG CAC CAG AAC CAG TGG TAT ACC GTG TGC CAG ACA 596  
 Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr Thr Val Cys Gln Thr  
 150 155 160 165  
 GGC TGG AGC CTC CGG GCC GCA AAG GTG GTG TGC CGG CAG CTG GGA TGT 644  
 Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys Arg Gln Leu Gly Cys  
 170 175 180  
 GGG AGG GCT GTA CTG ACT CAA AAA CGC TGC AAC AAG CAT GCC TAT GGC 692  
 Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn Lys His Ala Tyr Gly  
 185 190 195  
 CGA AAA CCC ATC TGG CTG AGC CAG ATG TCA TGC TCA GGA CGA GAA GCA 740  
 Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys Ser Gly Arg Glu Ala



140

200 205 210  
 ACC CTT CAG GAT TGC CCT TCT GGG CCT TGG GGG AAG AAC ACC TGC AAC 788  
 Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly Lys Asn Thr Cys Asn  
 215 220 225  
 CAT GAT GAA GAC ACG TGG GTC GAA TGT GAA GAT CCC TTT GAC TTG AGA 836  
 His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp Pro Phe Asp Leu Arg  
 230 235 240 245  
 CTA GTA GGA GGA GAC AAC CTC TGC TCT GGG CGA CTG GAG GTG CTG CAC 884  
 Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg Leu Glu Val Leu His  
 250 255 260  
 AAG GGC GTA TGG GGC TCT GTC TGT GAT GAC AAC TGG GGA GAA AAG GAG 932  
 Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn Trp Gly Glu Lys Glu  
 265 270 275  
 GAC CAG GTG GTA TGC AAG CAA CTG GGC TGT GGG AAG TCC CTC TCT CCC 980  
 Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly Lys Ser Leu Ser Pro  
 280 285 290  
 TCC TTC AGA GAC CGG AAA TGC TAT GGC CCT GGG GTT GGC CGC ATC TGG 1028  
 Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly Val Gly Arg Ile Trp  
 295 300 305  
 CTG GAT AAT GTT CGT TGC TCA GGG GAG GAG CAG TCC CTG GAG CAG TGC 1076  
 Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln Ser Leu Glu Gln Cys  
 310 315 320 325  
 CAG CAC AGA TTT TGG GGG TTT CAC GAC TGC ACC CAC CAG GAA GAT GTG 1124  
 Gln His Arg Phe Trp Gly Phe His Asp Cys Thr His Gln Glu Asp Val  
 330 335 340  
 GCT GTC ATC TGC TCA GGA TAGTATCCTG GTGTTGCTTG ACCTGGCC 1170  
 Ala Val Ile Cys Ser Gly  
 345  
 CCCCTGGCCC CGCCTGCCCT CTGCTTGTTT TCCTGAGCCC TGATTATCCT CATACTCATT 1230  
 CTGGGGCTCA GGCTTGAGCC ACTACTCCCT CATCCCCTCA GGAGTCTGAA CACTGGGCTT 1290  
 ATGCCTTACT CTCAGGGACA AGCAGCCCCC ATTGCTGCCT GTAGATGTGA GCTGTTGAGT 1350  
 TCCCTCTTGC TGGGGAAGAT GAGCTTCCAT GTATCCTGTG CTCAACCCTG ACCCTTTGAC 1410  
 ACTGGTTCTG GCCTTTCCTG CCTTTTCTCA AGCTGCCTGG AATCCTCAAA CCTGTCACTT 1470  
 TGGTCAGATG TGCAGACCAT TACTAAGGTC TATGTCTGCA AACATTACTA ATCTAGGTCC 1530  
 TATTACTAAT CTATGTCTGC AAACATTAAA GGAATGAAAC AATGAAAGGA ACATTGAAA 1590  
 1591  
 G

Sequence No.: 55

Sequence length: 1888

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

## Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP01293

## Sequence characteristics

Code representing characteristics: CDS

Existence site: 90.. 1754

Characterization method: E

## Sequence description

CCTTTTCAAA GATCTCTGAG GGAGACATTG CACCTGGCCA CTGCAGCCCA GAGCAGGTCT 60  
 GGCCACGGCC ATGAGCATGC TGAGCCATC ATG CCC ACC GTG GAT GAC ATT CTG 113  
 Met Pro Thr Val Asp Asp Ile Leu  
 1 5  
 GAG CAG GTT GGG GAG TCT GGC TGG TTC CAG AAG CAA GCC TTC CTC ATC 161  
 Glu Gln Val Gly Glu Ser Gly Trp Phe Gln Lys Gln Ala Phe Leu Ile  
 10 15 20  
 TTA TGC CTG CTG TCG GCT GCC TTT GCG CCC ATC TGT GTG GGC ATC GTC 209  
 Leu Cys Leu Leu Ser Ala Ala Phe Ala Pro Ile Cys Val Gly Ile Val  
 25 30 35 40  
 TTC CTG GGT TTC ACA CCT GAC CAC CAC TGC CAG AGT CCT GGG GTG GCT 257  
 Phe Leu Gly Phe Thr Pro Asp His His Cys Gln Ser Pro Gly Val Ala  
 45 50 55  
 GAG CTG AGC CAG CGC TGT GGC TGG AGC CCT GCG GAG GAG CTG AAC TAT 305  
 Glu Leu Ser Gln Arg Cys Gly Trp Ser Pro Ala Glu Glu Leu Asn Tyr  
 60 65 70  
 ACA GTG CCA GGC CTG GGG CCC GCG GGC GAG GCC TTC CTT GGC CAG TGC 353  
 Thr Val Pro Gly Leu Gly Pro Ala Gly Glu Ala Phe Leu Gly Gln Cys  
 75 80 85  
 AGG CGC TAT GAA GTG GAC TGG AAC CAG AGC GCC CTC AGC TGT GTA GAC 401  
 Arg Arg Tyr Glu Val Asp Trp Asn Gln Ser Ala Leu Ser Cys Val Asp  
 90 95 100  
 CCC CTG GCT AGC CTG GCC ACC AAC AGG AGC CAC CTG CCG CTG GGT CCC 449  
 Pro Leu Ala Ser Leu Ala Thr Asn Arg Ser His Leu Pro Leu Gly Pro  
 105 110 115 120  
 TGC CAG GAT GGC TGG GTG TAT GAC ACG CCC GGC TCT TCC ATC GTC ACT 497  
 Cys Gln Asp Gly Trp Val Tyr Asp Thr Pro Gly Ser Ser Ile Val Thr  
 125 130 135  
 GAG TTC AAC CTG GTG TGT GCT GAC TCC TGG AAG CTG GAC CTC TTT CAG 545  
 Glu Phe Asn Leu Val Cys Ala Asp Ser Trp Lys Leu Asp Leu Phe Gln  
 140 145 150  
 TCC TGT TTG AAT GCG GGC TTC TTC TTT GGC TCT CTC GGT GTT GGC TAC 593  
 Ser Cys Leu Asn Ala Gly Phe Phe Phe Gly Ser Leu Gly Val Gly Tyr  
 155 160 165

142

TTT GCA GAC AGG TTT GGC CGT AAG CTG TGT CTC CTG GGA ACT GTG CTG	641
Phe Ala Asp Arg Phe Gly Arg Lys Leu Cys Leu Leu Gly Thr Val Leu	
170 175 180	
GTC AAC GCG GTG TCG GGC GTG CTC ATG GCC TTC TCG CCC AAC TAC ATG	689
Val Asn Ala Val Ser Gly Val Leu Met Ala Phe Ser Pro Asn Tyr Met	
185 190 195 200	
TCC ATG CTG CTC TTC CGC CTG CTG CAG GGC CTG GTC AGC AAG GGC AAC	737
Ser Met Leu Leu Phe Arg Leu Leu Gln Gly Leu Val Ser Lys Gly Asn	
205 210 215	
TGG ATG GCT GGC TAC ACC CTA ATC ACA GAA TTT GTT GGC TCG GGC TCC	785
Trp Met Ala Gly Tyr Thr Leu Ile Thr Glu Phe Val Gly Ser Gly Ser	
220 225 230	
AGA AGA ACG GTG GCG ATC ATG TAC CAG ATG GCC TTC ACG GTG GGC CTG	833
Arg Arg Thr Val Ala Ile Met Tyr Gln Met Ala Phe Thr Val Gly Leu	
235 240 245	
GTG GCG CTT ACC GGG CTG GCC TAC GCC CTG CCT CAC TGG CGC TGG CTG	881
Val Ala Leu Thr Gly Leu Ala Tyr Ala Leu Pro His Trp Arg Trp Leu	
250 255 260	
CAG CTG GCA GTC TCC CTG CCC ACC TTC CTC TTC CTG CTC TAC TAC TGG	929
Gln Leu Ala Val Ser Leu Pro Thr Phe Leu Phe Leu Leu Tyr Tyr Trp	
265 270 275 280	
TGT GTG CCG GAG TCC CCT CGG TGG CTG TTA TCA CAA AAA AGA AAC ACT	977
Cys Val Pro Glu Ser Pro Arg Trp Leu Leu Ser Gln Lys Arg Asn Thr	
285 290 295	
GAA GCA ATA AAG ATA ATG GAC CAC ATC GCT CAA AAG AAT GGG AAG TTG	1025
Glu Ala Ile Lys Ile Met Asp His Ile Ala Gln Lys Asn Gly Lys Leu	
300 305 310	
CCT CCT GCT GAT TTA AAG ATG CTT TCC CTC GAA GAG GAT GTC ACC GAA	1073
Pro Pro Ala Asp Leu Lys Met Leu Ser Leu Glu Glu Asp Val Thr Glu	
315 320 325	
AAG CTG AGC CCT TCA TTT GCA GAC CTG TTC CGC ACG CCG CGC CTG AGG	1121
Lys Leu Ser Pro Ser Phe Ala Asp Leu Phe Arg Thr Pro Arg Leu Arg	
330 335 340	
AAG CGC ACC TTC ATC CTG ATG TAC CTG TGG TTC ACG GAC TCT GTG CTC	1169
Lys Arg Thr Phe Ile Leu Met Tyr Leu Trp Phe Thr Asp Ser Val Leu	
345 350 355 360	
TAT CAG GGG CTC ATC CTG CAC ATG GGC GCC ACC AGC GGG AAC CTC TAC	1217
Tyr Gln Gly Leu Ile Leu His Met Gly Ala Thr Ser Gly Asn Leu Tyr	
365 370 375	
CTG GAT TTC CTT TAC TCC GCT CTG GTC GAA ATC CCG GGG GCC TTC ATA	1265
Leu Asp Phe Leu Tyr Ser Ala Leu Val Glu Ile Pro Gly Ala Phe Ile	
380 385 390	
GCC CTC ATC ACC ATT GAC CGC GTG GGC CGC ATC TAC CCC ATG GCC GTG	1313
Ala Leu Ile Thr Ile Asp Arg Val Gly Arg Ile Tyr Pro Met Ala Val	

143

395	400	405	
TCA AAT TTG TTG GCG GGG GCA GCC TGC CTC GTC ATG ATT TTT ATC TCA			1361
Ser Asn Leu Leu Ala Gly Ala Ala Cys Leu Val Met Ile Phe Ile Ser			
410	415	420	
CCT GAC CTG CAC TGG TTA AAC ATC ATA ATC ATG TGT GTT GGC CGA ATG			1409
Pro Asp Leu His Trp Leu Asn Ile Ile Ile Met Cys Val Gly Arg Met			
425	430	435	440
GGA ATC ACC ATT GCA ATA CAA ATG ATC TGC CTG GTG AAT GCT GAG CTG			1457
Gly Ile Thr Ile Ala Ile Gln Met Ile Cys Leu Val Asn Ala Glu Leu			
445	450	455	
TAC CCC ACA TTC GTC AGG AAC CTC GGA GTG ATG GTG TGT TCC TCC CTG			1505
Tyr Pro Thr Phe Val Arg Asn Leu Gly Val Met Val Cys Ser Ser Leu			
460	465	470	
TGT GAC ATA GGT GGG ATA ATC ACC CCC TTC ATA GTC TTC AGG CTG AGG			1553
Cys Asp Ile Gly Gly Ile Ile Thr Pro Phe Ile Val Phe Arg Leu Arg			
475	480	485	
GAG GTC TGG CAA GCC TTG CCC CTC ATT TTG TTT GCG GTG TTG GGC CTG			1601
Glu Val Trp Gln Ala Leu Pro Leu Ile Leu Phe Ala Val Leu Gly Leu			
490	495	500	
CTT GCC GCG GGA GTG ACG CTA CTT CTT CCA GAG ACC AAG GGG GTC GCT			1649
Leu Ala Ala Gly Val Thr Leu Leu Leu Pro Glu Thr Lys Gly Val Ala			
505	510	515	520
TTG CCA GAG ACC ATG AAG GAC GCC GAG AAC CTT GGG AGA AAA GCA AAG			1697
Leu Pro Glu Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys			
525	530	535	
CCC AAA GAA AAC ACG ATT TAC CTT AAG GTC CAA ACC TCA GAA CCC TCG			1745
Pro Lys Glu Asn Thr Ile Tyr Leu Lys Val Gln Thr Ser Glu Pro Ser			
540	545	550	
GGC ACC TGAGAGAGAT GTTTTGC GGC GATGTCGTGT TGGAGGGATG AAGATGGAG			1800
Gly Thr			
TTATCCTCTG CAGAAATTCC TAGACGCCTT CACTTCTCTG TATTCTTCCT CATACTTGCC			1860
TACCCCAAAA TTAATATCAG TCCTAAAG			1888

Sequence No.: 56

Sequence length: 2033

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB  
 Clone name: HP10013  
 Sequence characteristics  
 Code representing characteristics: CDS  
 Existence site: 97.. 1149  
 Characterization method: E  
 Sequence description

GAGTCCGAGC GCGTCACCTC CTCACGCTGC GGCTGTCGCC CGTGTCCCGC CGGCCCGTTC	60
CGTGTGCCCC CGCAGTGCTG CGGCCGCCGC GGCACC ATG GCT GTG TTT GTC GTG	114
Met Ala Val Phe Val Val	
1 5	
CTC CTG GCG TTG GTG GCG GGT GTT TTG GGG AAC GAG TTT AGT ATA TTA	162
Leu Leu Ala Leu Val Ala Gly Val Leu Gly Asn Glu Phe Ser Ile Leu	
10 15 20	
AAA TCA CCA GGG TCT GTT GTT TTC CGA AAT GGA AAT TGG CCT ATA CCA	210
Lys Ser Pro Gly Ser Val Val Phe Arg Asn Gly Asn Trp Pro Ile Pro	
25 30 35	
GGA GAG CGG ATC CCA GAC GTG GCT GCA TTG TCC ATG GGC TTC TCT GTG	258
Gly Glu Arg Ile Pro Asp Val Ala Ala Leu Ser Met Gly Phe Ser Val	
40 45 50	
AAA GAA GAC CTT TCT TGG CCA GGA CTC GCA GTG GGT AAC CTG TTT CAT	306
Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala Val Gly Asn Leu Phe His	
55 60 65 70	
CGT CCT CGG GCT ACC GTC ATG GTG ATG GTG AAG GGA GTG AAC AAA CTG	354
Arg Pro Arg Ala Thr Val Met Val Met Val Lys Gly Val Asn Lys Leu	
75 80 85	
GCT CTA CCC CCA GGC AGT GTC ATT TCG TAC CCT TTG GAG AAT GCA GTT	402
Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr Pro Leu Glu Asn Ala Val	
90 95 100	
CCT TTT AGT CTT GAC AGT GTT GCA AAT TCC ATT CAC TCC TTA TTT TCT	450
Pro Phe Ser Leu Asp Ser Val Ala Asn Ser Ile His Ser Leu Phe Ser	
105 110 115	
GAG GAA ACT CCT GTT GTT TTG CAG TTG GCT CCC AGT GAG GAA AGA GTG	498
Glu Glu Thr Pro Val Val Leu Gln Leu Ala Pro Ser Glu Glu Arg Val	
120 125 130	
TAT ATG GTA GGG AAG GCA AAC TCA GTG TTT GAA GAC CTT TCA GTC ACC	546
Tyr Met Val Gly Lys Ala Asn Ser Val Phe Glu Asp Leu Ser Val Thr	
135 140 145 150	
TTG CGC CAG CTC CGT AAT CGC CTG TTT CAA GAA AAC TCT GTT CTC AGT	594
Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln Glu Asn Ser Val Leu Ser	
155 160 165	
TCA CTC CCC CTC AAT TCT CTG AGT AGG AAC AAT GAA GTT GAC CTG CTC	642
Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn Asn Glu Val Asp Leu Leu	

145  
170 175 180  
TTT CTT TCT GAA CTG CAA GTG CTA CAT GAT ATT TCA AGC TTG CTG TCT 690  
Phe Leu Ser Glu Leu Gln Val Leu His Asp Ile Ser Ser Leu Leu Ser  
185 190 195  
CGT CAT AAG CAT CTA GCC AAG GAT CAT TCT CCT GAT TTA TAT TCA CTG 738  
Arg His Lys His Leu Ala Lys Asp His Ser Pro Asp Leu Tyr Ser Leu  
200 205 210  
GAG CTG GCA GGT TTG GAT GAA ATT GGG AAG CGT TAT GGG GAA GAC TCT 786  
Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys Arg Tyr Gly Glu Asp Ser  
215 220 225 230  
GAA CAA TTC AGA GAT GCT TCT AAG ATC CTT GTT GAC GCT CTG CAA AAG 834  
Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu Val Asp Ala Leu Gln Lys  
235 240 245  
TTT GCA GAT GAC ATG TAC AGT CTT TAT GGT GGG AAT GCA GTG GTA GAG 882  
Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly Gly Asn Ala Val Val Glu  
250 255 260  
TTA GTC ACT GTC AAG TCA TTT GAC ACC TCC CTC ATT AGG AAG ACA AGG 930  
Leu Val Thr Val Lys Ser Phe Asp Thr Ser Leu Ile Arg Lys Thr Arg  
265 270 275  
ACT ATC CTT GAG GCA AAA CAA GCG AAG AAC CCA GCA AGT CCC TAT AAC 978  
Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn Pro Ala Ser Pro Tyr Asn  
280 285 290  
CTT GCA TAT AAG TAT AAT TTT GAA TAT TCC GTG GTT TTC AAC ATG GTA 1026  
Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser Val Val Phe Asn Met Val  
295 300 305 310  
CTT TGG ATA ATG ATC GCC TTG GCC TTG GCT GTG ATT ATC ACC TCT TAC 1074  
Leu Trp Ile Met Ile Ala Leu Ala Leu Val Ile Ile Thr Ser Tyr  
315 320 325  
AAT ATT TGG AAC ATG GAT CCT GGA TAT GAT AGC ATC ATT TAT AGG ATG 1122  
Asn Ile Trp Asn Met Asp Pro Gly Tyr Asp Ser Ile Ile Tyr Arg Met  
330 335 340  
ACA AAC CAG AAG ATT CGA ATG GAT TGAATGTTAC CTGTGCCAGA ATTA 1170  
Thr Asn Gln Lys Ile Arg Met Asp  
345 350  
GAAAAGGGGG TTGGAAATTG GCTGTTTTGT TAAAAATATAT CTTTTAGTGT GCTTTAAAGT 1230  
AGATAGTATA CTTTACATTT ATAAAAAAA ATCAAATTTT GTTCTTTATT TTGTGTGTGC 1290  
CTGTGATGTT TTTCTAGAGT GAATTATAGT ATTGACGTGA ATCCCACTGT GGTATAGATT 1350  
CCATAATATG CTTGAATATT ATGATATAGC CATTTAATAA CATTGATTTT ATTCTGTTTA 1410  
ATGAATTTGG AAATATGCAC TGAAAGAAAT GTAAACATT TAGAATAGCT CGTGTATG 1470  
AAAAAGTGC ACTGAATTTA TTAGACAAAC TTACGAATGC TTAACCTCTT TACACAGCAT 1530  
AGGTGAAAAT CATATTTGGG CTATTGTATA CTATGAACAA TTTGTAAATG TCTTAATTTG 1590  
ATGTAAATAA CTCTGAAACA AGAGAAAAGG TTTTAACTT AGAGTAGCCC TAAAAATATG 1650  
ATGTGCTTAT ATAATCGCTT AGTTTTGGAA CTGTATCTGA GTAACAGAGG ACAGCTGTTT 1710  
TTTAACCTC TTCTGCAAGT TTGTTGACCT ACATGGGCTA ATATGGATAC TAAAAATACT 1770

ACATTGATCT AAGAAGAAAC TAGCCTTGTG GAGTATATAG ATGCTTTTCA TTATACACAC 1830  
 AAAAATCCCT GAGGGACATT TTGAGGCATG AATATAAAAC ATTTTATTT CAGTAACTTT 1890  
 TCCCCCTGTG TAAGTTACTA TGGTTTGTGG TACAACTTCA TTCTATAGAA TATTAAGTGG 1950  
 AAGTGGGTGA ATTCTACTTT TTATGTTGGA GTGGACCAAT GTCTATCAAG AGTGACAAAT 2010  
 AAAGTTAATG ATGATTCCAA AAC 2033

Sequence No.: 57

Sequence length: 911

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10034

Sequence characteristics

Code representing characteristics: CDS

Existence site: 176.. 805

Characterization method: E

Sequence description

ACGCCTGGGT GACCTCTACG TATATACAGA GCCTCCCTGG CCCTCCTGGA AAGAGTCCTG 60  
 GAAAGACAAC CTCAGGTCC AGCCCTGGAG CTGGAGGAGT GGAGCCCCAC TCTGAAGACG 120  
 CAGCCTTTCT CCAGGTTCTG TCTCTCCCAT TCTGATTCTT GACACCAGAT GCAGG ATG 178  
 Met  
 1  
 GTG TCC TCT CCC TGC ACG CAG GCA AGC TCA CGG ACT TGC TCC CGT ATC 226  
 Val Ser Ser Pro Cys Thr Gln Ala Ser Ser Arg Thr Cys Ser Arg Ile  
 5 10 15  
 CTG GGA CTG AGC CTT GGG ACT GCA GCC CTG TTT GCT GCT GGG GCC AAC 274  
 Leu Gly Leu Ser Leu Gly Thr Ala Ala Leu Phe Ala Ala Gly Ala Asn  
 20 25 30  
 GTG GCA CTC CTC CTT CCT AAC TGG GAT GTC ACC TAC CTG TTG AGG GGC 322  
 Val Ala Leu Leu Leu Pro Asn Trp Asp Val Thr Tyr Leu Leu Arg Gly  
 35 40 45  
 CTC CTT GGC AGG CAT GCC ATG CTG GGA ACT GGG CTC TGG GGA GGA GGC 370  
 Leu Leu Gly Arg His Ala Met Leu Gly Thr Gly Leu Trp Gly Gly Gly  
 50 55 60 65  
 CTC ATG GTA CTC ACT GCA GCT ATC CTC ATC TCC TTG ATG GGC TGG AGA 418  
 Leu Met Val Leu Thr Ala Ala Ile Leu Ile Ser Leu Met Gly Trp Arg

147

70	75	80	
TAC GGC TGC TTC AGT AAG AGT GGG CTC TGT CGA AGC GTG CTT ACT GCT			466
Tyr Gly Cys Phe Ser Lys Ser Gly Leu Cys Arg Ser Val Leu Thr Ala			
85	90	95	
CTG TTG TCA GGT GGC CTG GCT TTA CTT GGA GCC CTG ATT TGC TTT GTC			514
Leu Leu Ser Gly Gly Leu Ala Leu Leu Gly Ala Leu Ile Cys Phe Val			
100	105	110	
ACT TCT GGA GTT GCT CTG AAA GAT GGT CCT TTT TGC ATG TTT GAT GTT			562
Thr Ser Gly Val Ala Leu Lys Asp Gly Pro Phe Cys Met Phe Asp Val			
115	120	125	
TCA TCC TTC AAT CAG ACA CAA GCT TGG AAA TAT GGT TAC CCA TTC AAA			610
Ser Ser Phe Asn Gln Thr Gln Ala Trp Lys Tyr Gly Tyr Pro Phe Lys			
130	135	140	
GAC CTG CAT AGT AGG AAT TAT CTG TAT GAC CGT TCG CTC TGG AAC TCC			658
Asp Leu His Ser Arg Asn Tyr Leu Tyr Asp Arg Ser Leu Trp Asn Ser			
150	155	160	
GTC TGC CTG GAG CCC TCT GCA GCT GTT GTC TGG CAC GTG TCC CTC TTC			706
Val Cys Leu Glu Pro Ser Ala Ala Val Val Trp His Val Ser Leu Phe			
165	170	175	
TCC GCC CTT CTG TGC ATC AGC CTG CTC CAG CTT CTC CTG GTG GTC GTT			754
Ser Ala Leu Leu Cys Ile Ser Leu Leu Gln Leu Leu Leu Val Val Val			
180	185	190	
CAT GTC ATC AAC AGC CTC CTG GGC CTT TTC TGC AGC CTC TGC GAG AAG			802
His Val Ile Asn Ser Leu Leu Gly Leu Phe Cys Ser Leu Cys Glu Lys			
195	200	205	
TGACAGGC AGAACCTTCA CTTGCAAGCA TGGGTGTTTA TCATCATCGG CTGTCTTGAA			860
TCCTTTCTAC AAGGAGTGGG TACGAATTAT AAACAACTT CCCCTTTAGG T			911

Sequence No.: 58

Sequence length: 601

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10050

Sequence characteristics

Code representing characteristics: CDS

Existence site: 10.. 501

Characterization method: E



148

## Sequence description

CCATCTGTC ATG GCG GCT GGG CTG TTT GGT TTG AGC GCT CGC CGT CTT TTG 51  
 Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu  
 1 5 10  
 GCG GCA GCG GCG ACG CGA GGG CTC CCG GCC GCC CGC GTC CGC TGG GAA 99  
 Ala Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu  
 15 20 25 30  
 TCT AGC TTC TCC AGG ACT GTG GTC GCC CCG TCC GCT GTG GCG GGA AAG 147  
 Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys  
 35 40 45  
 CGG CCC CCA GAA CCG ACC ACA CCG TGG CAA GAG GAC CCA GAA CCC GAG 195  
 Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu  
 50 55 60  
 GAC GAA AAC TTG TAT GAG AAG AAC CCA GAC TCC CAT GGT TAT GAC AAG 243  
 Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys  
 65 70 75  
 GAC CCC GTT TTG GAC GTC TGG AAC ATG CGA CTT GTC TTC TTC TTT GGC 291  
 Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly  
 80 85 90  
 GTC TCC ATC ATC CTG GTC CTT GGC AGC ACC TTT GTG GCC TAT CTG CCT 339  
 Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro  
 95 100 105 110  
 GAC TAC AGG TGC ACA GGG TGT CCA AGA GCG TGG GAT GGG ATG AAA GAG 387  
 Asp Tyr Arg Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu  
 115 120 125  
 TGG TCC CGC CGC GAA GCT GAG AGG CTT GTG AAA TAC CGA GAG GCC AAT 435  
 Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn  
 130 135 140  
 GGC CTT CCC ATC ATG GAA TCC AAC TGC TTC GAC CCC AGC AAG ATC CAG 483  
 Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln  
 145 150 155  
 CTG CCA GAG GAT GAG TGACCAGTTG CTAAGTGGGG CTCAAGAAGC AC 530  
 Leu Pro Glu Asp Glu  
 160  
 CGCCTTCCCC ACCCCCTGCC TGCCATTCTG ACCTCTTCTC AGAGCACCTA ATTAAAGGGG 590  
 CTGAAAGTCT G 601

Sequence No.: 59

Sequence length: 394

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10071

Sequence characteristics

Code representing characteristics: CDS

Existence site: 47.. 325

Characterization method: E

Sequence description

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AACATCCGGG CCGCGCGGGG AAGGGGAGAC GTGGGGTAGA GTGACC ATG ACG AAA      55
                                         Met Thr Lys
                                         1
TTA GCG CAG TGG CTT TGG GGA CTA GCG ATC CTG GGC TCC ACC TGG GTG      103
Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser Thr Trp Val
      5              10              15
GCC CTG ACC ACG GGA GCC TTG GGC CTG GAG CTG CCC TTG TCC TGC CAG      151
Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu Ser Cys Gln
      20              25              30              35
GAA GTC CTG TGG CCA CTG CCC GCC TAC TTG CTG GTG TCC GCC GCC TGC      199
Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser Ala Gly Cys
      40              45              50
TAT GCC CTG GGC ACT GTG GGC TAT CGT GTG GCC ACT TTT CAT GAC TGC      247
Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe His Asp Cys
      55              60              65
GAG GAC GCC GCA CGC GAG CTG CAG AGC CAG ATA CAG GAG GCC CGA GCC      295
Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu Ala Arg Ala
      70              75              80
GAC TTA GCC CGC AGG GGG CTG CGC TTC TGACAGCCTA ACCCCATT      340
Asp Leu Ala Arg Arg Gly Leu Arg Phe
      85              90
CCTGTGCGGA CAGCCCTTCC TCCCATTTC CATTAAAGAG CCAGTTTATT TTCT      394

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Sequence No.: 60

Sequence length: 732

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10076

Sequence characteristics

Code representing characteristics: CDS

Existence site: 82.. 600

Characterization method: E

Sequence description

AGAAACGTGT TCGCTGCCCA GAAGAAGGGA AGGCGCGAGT GAGGAAAGGA GGTACTGTAG 60  
 ATGCCCTCCA AATCCTTGGT T ATG GAA TAT TTG GCT CAT CCC AGT ACA CTC 111  
 Met Glu Tyr Leu Ala His Pro Ser Thr Leu  
 1 5 10  
 GGC TTG GCT GTT GGA GTT GCT TGT GGC ATG TGC CTG GGC TGG AGC CTT 159  
 Gly Leu Ala Val Gly Val Ala Cys Gly Met Cys Leu Gly Trp Ser Leu  
 15 20 25  
 CGA GTA TGC TTT GGG ATG CTC CCC AAA AGC AAG ACG AGC AAG ACA CAC 207  
 Arg Val Cys Phe Gly Met Leu Pro Lys Ser Lys Thr Ser Lys Thr His  
 30 35 40  
 ACA GAT ACT GAA AGT GAA GCA AGC ATC TTG GGA GAC AGC GGG GAG TAC 255  
 Thr Asp Thr Glu Ser Glu Ala Ser Ile Leu Gly Asp Ser Gly Glu Tyr  
 45 50 55  
 AAG ATG ATT CTT GTG GTT CGA AAT GAC TTA AAG ATG GGA AAA GGG AAA 303  
 Lys Met Ile Leu Val Val Arg Asn Asp Leu Lys Met Gly Lys Gly Lys  
 60 65 70  
 GTG GCT GCC CAG TGC TCT CAT GCT GCT GTT TCA GCC TAC AAG CAG ATT 351  
 Val Ala Ala Gln Cys Ser His Ala Ala Val Ser Ala Tyr Lys Gln Ile  
 75 80 85 90  
 CAA AGA AGA AAT CCT GAA ATG CTC AAA CAA TGG GAA TAC TGT GGC CAG 399  
 Gln Arg Arg Asn Pro Glu Met Leu Lys Gln Trp Glu Tyr Cys Gly Gln  
 95 100 105  
 CCC AAG GTG GTG GTC AAA GCT CCT GAT GAA GAA ACC CTG ATT GCA TTA 447  
 Pro Lys Val Val Val Lys Ala Pro Asp Glu Glu Thr Leu Ile Ala Leu  
 110 115 120  
 TTG GCC CAT GCA AAA ATG CTG GGA CTG ACT GTA AGT TTA ATT CAA GAT 495  
 Leu Ala His Ala Lys Met Leu Gly Leu Thr Val Ser Leu Ile Gln Asp  
 125 130 135  
 GCT GGA CGT ACT CAG ATT GCA CCA GGC TCT CAA ACT GTC CTA GGG ATT 543  
 Ala Gly Arg Thr Gln Ile Ala Pro Gly Ser Gln Thr Val Leu Gly Ile  
 140 145 150  
 GGG CCA GGA CCA GCA GAC CTA ATT GAC AAA GTC ACT GGT CAC CTA AAA 591  
 Gly Pro Gly Pro Ala Asp Leu Ile Asp Lys Val Thr Gly His Leu Lys  
 155 160 165 170  
 CTT TAC TAGGTGGACT TTGATATGAC AACAAACCCT CCATCACAAG TGT 640  
 Leu Tyr

TTGAAGCCTG TCAGATTCTA ACAACAAAAG CTGAATTTCT TCACCCAAC TAAATGTTCT 700  
 TGAGATGAAA ATAAACCTA TTCCCATGTT CT 732

Sequence No.: 61  
 Sequence length: 697  
 Sequence type: Nucleic acid  
 Strandedness: Double  
 Topology: Linear  
 Sequence kind: cDNA to mRNA  
 Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10085

Sequence characteristics

Code representing characteristics: CDS

Existence site: 151.. 600

Characterization method: E

Sequence description

TATACCTCTA GTTGGAGCT GTGCTGTAAA AACAAGAGTA ACATTTTAT ATTAAAGTTA 60  
 AATAAGTTA CAACTTTGAA GAGAGTTTCT GCAAGACATG ACACAAAGCT GCTAGCAGAA 120  
 AATCAAAACG CTGATTAAAA GAAGCACGGT ATG ATG ACC AAA CAT AAA AAG TGT 174  
 Met Met Thr Lys His Lys Lys Cys  
 1 5  
 TTT ATA ATT GTT GGT GTT TTA ATA ACA ACT AAT ATT ATT ACT CTG ATA 222  
 Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile  
 10 15 20  
 GTT AAA CTA ACT CGA GAT TCT CAG AGT TTA TGC CCC TAT GAT TGG ATT 270  
 Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile  
 25 30 35 40  
 GGT TTC CAA AAC AAA TGC TAT TAT TTC TCT AAA GAA GAA GGA GAT TGG 318  
 Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp  
 45 50 55  
 AAT TCA AGT AAA TAC AAC TGT TCC ACT CAA CAT GCC GAC CTA ACT ATA 366  
 Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile  
 60 65 70  
 ATT GAC AAC ATA GAA GAA ATG AAT TTT CTT AGG CGG TAT AAA TGC AGT 414  
 Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser  
 75 80 85  
 TCT GAT CAC TGG ATT GGA CTG AAG ATG GCA AAA AAT CGA ACA GGA CAA 462  
 Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln

152

90	95	100	510
TGG GTA GAT GGA GCT ACA TTT ACC AAA TCG TTT GGC ATG AGA GGG AGT			
Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser			
105	110	115	120
GAA GGA TGT GCC TAC CTC AGC GAT GAT GGT GCA GCA ACA GCT AGA TGT			558
Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys			
125	130	135	
TAC ACC GAA AGA AAA TGG ATT TGC AGG AAA AGA ATA CAC TAA			600
Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His			
140	145		
GTAAATGTCT AAGATAATGG GGAAAATAGA AAATAACATT ATTAAGTGTA AAACCAGCAA			660
AGTACTTTTT TAATTAAACA AAGTTCGAGT TTTGTAC			697

Sequence No.: 62

Sequence length: 1186

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10122

Sequence characteristics

Code representing characteristics: CDS

Existence site: 139.. 705

Characterization method: E

Sequence description

AAGTGCGATC TTCGGGCTGT CAGAGTTGGT CTGTTACTCG GTGGTGGCGG AGTCTACGGA	60
AGCCGTTTTTC GCTTCACTTT TCCTGGCTGT AGAGCGCTTT CCCCCTGGCG GGTGAGAGTG	120
CAGAGACGAA GGTGCGAG ATG AGC ACT ATG TTC GCG GAC ACT CTC CTC ATC	171
Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile	
1 5 10	
GTT TTT ATC TCT GTG TGC ACG GCT CTG CTC GCA GAG GGC ATA ACC TGG	219
Val Phe Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp	
15 20 25	
GTC CTG GTT TAC AGG ACA GAC AAG TAC AAG AGA CTG AAG GCA GAA GTG	267
Val Leu Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val	
30 35 40	
GAA AAA CAG AGT AAA AAA TTG GAA AAG AAG AAG GAA ACA ATA ACA GAG	315
Glu Lys Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu	
45 50 55	

153

TCA GCT GGT CGA CAA CAG AAA AAG AAA ATA GAG AGA CAA GAA GAG AAA 363  
 Ser Ala Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Gln Glu Glu Lys  
 60 65 70 75  
 CTG AAG AAT AAC AAC AGA GAT CTA TCA ATG GTT CGA ATG AAA TCC ATG 411  
 Leu Lys Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met  
 80 85 90  
 TTT GCT ATT GGC TTT TGT TTT ACT GCC CTA ATG GGA ATG TTC AAT TCC 459  
 Phe Ala Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser  
 95 100 105  
 ATA TTT GAT GGT AGA GTG GTG GCA AAG CTT CCT TTT ACC CCT CTT TCT 507  
 Ile Phe Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser  
 110 115 120  
 TAC ATC CAA GGA CTG TCT CAT CGA AAT CTG CTG GGA GAT GAC ACC ACA 555  
 Tyr Ile Gln Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr  
 125 130 135  
 GAC TGT TCC TTC ATT TTC CTG TAT ATT CTC TGT ACT ATG TCG ATT CGA 603  
 Asp Cys Ser Phe Ile Phe Leu Tyr Ile Leu Cys Thr Met Ser Ile Arg  
 140 145 150 155  
 CAG AAC ATT CAG AAG ATT CTC GGC CTT GCC CCT TCA CGA GCC GCC ACC 651  
 Gln Asn Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr  
 160 165 170  
 AAG CAG GCA GGT GGA TTT CTT GGC CCA CCA CCT CCT TCT GGG AAG TTC 699  
 Lys Gln Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe  
 175 180 185  
 TCT TGA ACT CAAG AACTCTTTAT TTTCTATCAT TCTTTCTAGA CACACACA 750  
 Ser  
 CATCAGACTG GCAACTGTTT TG TAGCAAGA GCCATAGGTA GCCTTACTAC TTGGGCCTCT 810  
 TTCTAGTTTT GAATTATTTT TAAGCCTTTT GGGTATGATT AGAGTGAAAA TGGCAGCCAG 870  
 CAAACTTGAT AGTGCTTTTG GTCCTAGATG ATTTTATCA AATAAGTGGA TTGATTAGTT 930  
 AAGTTCAGGT AATGTTTATG TAATGAAAAA CAAATAGCAT CCTTCTTGTT TCATTTACAT 990  
 AAGTATTTTC TGTGGGACCG ACTCTCAAGG CACTGTGTAT GCCCTGCAAG TTGGCTGTCT 1050  
 ATGAGCATTT AGAGATTTAG AAGAAAAATT TAGTTTGTGT AACCCTTGTA ACTGTTTGT 1110  
 TTGTTGTTGT TTTTTTTTCA AGCCAAATAC ATGACATAAG ATCAATAAAG AGGCCAAATT 1170  
 TTTAGCTGTT TTATGT 1186

Sequence No.: 63

Sequence length: 1409

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Lymphoma

Cell line: U937

Clone name: HP10136

# Sequence characteristics

Code representing characteristics: CDS

Existence site: 82.. 729

Characterization method: E

## Sequence description

ATAACTGTTG TCGCGGCGGA GGAAGTGAGG ACGGCGCCAA GGGCCTTCCG GGCCAGTGT	60
GGATCCCTGT AGTTTGTGAA G ATG GTG TTG CTA ACA ATG ATC GCC CGA GTG	111
Met Val Leu Leu Thr Met Ile Ala Arg Val	
1 5 10	
GCG GAC GGG CTC CCG CTG GCC GCC TCG ATG CAG GAG GAC GAA CAG TCT	159
Ala Asp Gly Leu Pro Leu Ala Ala Ser Met Gln Glu Asp Glu Gln Ser	
15 20 25	
GGC CGG GAC CTT CAA CAG TAT CAG AGT CAG GCT AAG CAA CTC TTT CGA	207
Gly Arg Asp Leu Gln Gln Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg	
30 35 40	
AAG TTG AAT GAA CAG TCC CCT ACC AGA TGT ACC TTG GAA GCA GGA GCC	255
Lys Leu Asn Glu Gln Ser Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala	
45 50 55	
ATG ACT TTT CAC TAC ATT ATT GAG CAG GGG GTG TGT TAT TTG GTT TTA	303
Met Thr Phe His Tyr Ile Ile Glu Gln Gly Val Cys Tyr Leu Val Leu	
60 65 70	
TGT GAA GCT GCC TTC CCT AAG AAG TTG GCT TTT GCC TAC CTA GAA GAT	351
Cys Glu Ala Ala Phe Pro Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp	
75 80 85 90	
TTG CAC TCA GAA TTT GAT GAA CAG CAT GGA AAG AAG GTG CCC ACT GTG	399
Leu His Ser Glu Phe Asp Glu Gln His Gly Lys Lys Val Pro Thr Val	
95 100 105	
TCC CGA CCC TAT TCC TTT ATT GAA TTT GAT ACT TTC ATT CAG AAA ACC	447
Ser Arg Pro Tyr Ser Phe Ile Glu Phe Asp Thr Phe Ile Gln Lys Thr	
110 115 120	
AAG AAG CTC TAC ATT GAC AGT CGT GCT CGA AGA AAT CTA GGC TCC ATC	495
Lys Lys Leu Tyr Ile Asp Ser Arg Ala Arg Arg Asn Leu Gly Ser Ile	
125 130 135	
AAC ACT GAA TTG CAA GAT GTG CAG AGG ATC ATG GTG GCC AAT ATT GAA	543
Asn Thr Glu Leu Gln Asp Val Gln Arg Ile Met Val Ala Asn Ile Glu	
140 145 150	
GAA GTG TTA CAA CGA GGA GAA GCA CTC TCA GCA TTG GAT TCA AAG GCT	591
Glu Val Leu Gln Arg Gly Glu Ala Leu Ser Ala Leu Asp Ser Lys Ala	
155 160 165 170	

155

AAC AAT TTG TCC AGT CTG TCC AAG AAA TAC CGC CAG GAT GCG AAG TAC	639
Asn Asn Leu Ser Ser Leu Ser Lys Lys Tyr Arg Gln Asp Ala Lys Tyr	
175 180 185	
TTG AAC ATG CGT TCC ACT TAT GCC AAA CTT GCA GCA GTA GCT GTA TTT	687
Leu Asn Met Arg Ser Thr Tyr Ala Lys Leu Ala Ala Val Ala Val Phe	
190 195 200	
TTC ATC ATG TTA ATA GTG TAT GTC CGA TTC TGG TGG CTG TGAA	730
Phe Ile Met Leu Ile Val Tyr Val Arg Phe Trp Trp Leu	
205 210 215	
ATAATGAATA CAGTCACTGG TAAGGGAGAA CCTAGAACCC AGTAGGTGTA TATTTTCAGG	790
AAACTGAGCT CACAGAGATG TGTATTAGAA TCCAAGTGGA ACTTCTGCCT CTAAAGACCT	850
TGCAAGAAAA GAGATGCCCT GAAAATGAAA GGTTCACCT CATTTAATGA AGCTTAACCC	910
TATGTAGAAA GTCTCTTTTCG GGGGCAGAGG CTTTCTCTGG GTGCCAAGCC ATATATATTA	970
GGGAATAGTA GATTGTTAAT TTCGTTTTTTT CCCTCCCAGT GCATTTTAAA AACAGCACTG	1030
GCTGGGGCAT TCTCATTCTC TGATGGAGCC ATCAATGAGA TTAACTTAG TCAACCTGTG	1090
CTAGCAACAT TCTGAAATTC CTTCAAAGAA GGCAGTCCTT TGGGAAGGTG TTTTTTTTTT	1150
TTTTTTTTTTT TTTGACTCTA ATCAACATTC CTTTGTGTTG TGACATTTGT GATTTTCAGT	1210
AATCTGAGTT TTTGATGGCC TTTTAAACAA GACTCCAGTA TGTGAAGGTT AATTGCTGTG	1270
CTCCACAGAT CTTGTCTATT GGCCCCGTGTA GAAAGTTAAC CTTTGTGTTT TCCCTTTTAT	1330
AATTTGCTTA TTGCACAATT GCTTTAGGGT AAGTGAATTA TATTAAGATG CCTTGAAATT	1390
ATAGCACTCC TTGATTAAG	1409

Sequence No.: 64

Sequence length: 974

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10175

Sequence characteristics

Code representing characteristics: CDS

Existence site: 174.. 512

Characterization method: E

Sequence description

AGAGCCGCTC CCCTCTCCTC GCCCCGCCAC CGGGACGGAG AGCGCCCGCC GCTGCATTTT	60
CGGCGACACC TCGCAGTCAT TCCTGCGGCT TCGCGCGCCCT TGTAGACAGC CGGGGCCTTC	120
GTGAGACCGG TGCAGGCCTG GGGTAGTCTC CTGTCTGGAC AGAGAAGAGA AAA ATG	176
Met	



Year	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Sequence No.: 65  
Sequence length: 925  
Sequence type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Sequence kind: cDNA to mRNA  
Original source:  
Organism species: *Homo sapiens*  
Cell kind: Epidermoid carcinoma  
Cell line: KB  
Clone name: HP10179  
Sequence characteristics  
Code representing characteristics: CDS

157

Existence site: 122.. 466

Characterization method: E

Sequence description

AATCGCGTTT CCGGAGAGAC CTGGCTGCTG TGTCCGCGG CTTGCGCTCC GTAGTGGACT	60
CCGCGGGCCT TCGGCAGATG CAGGCCTGGG GTAGTCTCCT TTCTGGACTG AGAAGAGAAG	120
ATG GAG AAG CCC CTC TTC CCA TTA GTG CCT TTG CAT TGG TTT GGC TTT	168
Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe	
1 5 10 15	
GGC TAC ACA GCA CTG GTT GTT TCT GGT GGG ATC GTT GGC TAT GTA AAA	216
Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys	
20 25 30	
ACA GGC AGC GTG CCG TCC CTG GCA GCA GGG CTG CTC TTC GGC AGT CTA	264
Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu	
35 40 45	
GCC GGC CTG GGT GCT TAC CAG CTG TAT CAG GAT CCT AGG AAC GTT TGG	312
Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp	
50 55 60	
GGT TTC CTA GCC GCT ACA TCT GTT ACT TTT GTT GGT GTT ATG GGA ATA	360
Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly Met	
65 70 75 80	
AGA TCC TAC TAC TAT GGA AAA TTC ATG CCT GTA GGT TTA ATT GCA GGT	408
Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala Gly	
85 90 95	
GCC AGT TTG CTG ATG GCC GCC AAA GTT GGA GTT CGT ATG TTG ATG ACA	456
Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met Thr	
100 105 110	
TCT GAT TAGCAGAAGT CATGTTGCA GCTTGGACTC ATGAAGGATT AAAAAATCT	510
Ser Asp	
GCATCTTCCA CTATTTTCAA TGTATTAAGA GAAATAAGTG CAGCATTTTT GCATCTGACA	570
TTTTACCTAA AAAAAAAAAAG ACACCAAATT TGGCGGAGGG GTGAAAAATC AGTTGTTACC	630
ATTATAACCC TACAGAGGTG GTGAGCATGT AACATGAGCT TATTGAGACC ATCATAGAGA	690
TCGATTCTTG TATATTGATT TTATCTCTTT CTGTATCTAT AGGTAAATCT CAAGGGTAAA	750
ATGTTAGGTG TTGACATTGA GAACCCGTGAA ACCCCATTCC CTGCTCAGAG GAACAGTGTG	810
AAAAAAAATC TCTTGAGAGA TTTAGAATAT CTTTTCTTTT GCTCATCTTA GACCACAGAC	870
TGACTTTGAA ATTATGTTAA GTGAAATATC AATGAAAATA AAGTTTACTA TAAAT	925

Sequence No.: 66

Sequence length: 1115

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

Cell line: HT-1080

Clone name: HP10196

Sequence characteristics

Code representing characteristics: CDS

Existence site: 10.. 993

Characterization method: E

Sequence description

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GCGGGGAAA ATG GCG GCG GCG GCG GCG GCG GCT GCA GCT ACG AAC GGG ACC      51
      Met Ala Ala Ala Ala Ala Ala Ala Ala Ala Thr Asn Gly Thr
              1              5              10
GGA GGA AGC AGC GGG ATG GAG GTG GAT GCA GCA GTA GTC CCC AGC GTG      99
Gly Gly Ser Ser Gly Met Glu Val Asp Ala Ala Val Val Pro Ser Val
      15              20              25              30
ATG GCC TGC GGA GTG ACT GGG AGT GTT TCC GTC GCT CTC CAT CCC CTT      147
Met Ala Cys Gly Val Thr Gly Ser Val Ser Val Ala Leu His Pro Leu
              35              40              45
GTC ATT CTC AAC ATC TCA GAC CAC TGG ATC CGC ATG CGC TCC CAG GAG      195
Val Ile Leu Asn Ile Ser Asp His Trp Ile Arg Met Arg Ser Gln Glu
              50              55              60
GGG CGG CCT GTG CAG GTG ATT GGG GCT CTG ATT GGC AAG CAG GAG GGC      243
Gly Arg Pro Val Gln Val Ile Gly Ala Leu Ile Gly Lys Gln Glu Gly
              65              70              75
CGA AAT ATC GAG GTG ATG AAC TCC TTT GAG CTG CTG TCC CAC ACC GTG      291
Arg Asn Ile Glu Val Met Asn Ser Phe Glu Leu Leu Ser His Thr Val
              80              85              90
GAA GAG AAG ATT ATC ATT GAC AAG GAA TAT TAT TAC ACC AAG GAG GAG      339
Glu Glu Lys Ile Ile Ile Asp Lys Glu Tyr Tyr Tyr Thr Lys Glu Glu
              95              100              105              110
CAG TTT AAA CAG GTG TTC AAG GAG CTG GAG TTT CTG GGT TGG TAT ACC      387
Gln Phe Lys Gln Val Phe Lys Glu Leu Glu Phe Leu Gly Trp Tyr Thr
              115              120              125
ACA GGG GGG CCA CCT GAC CCC TCG GAC ATC CAC GTC CAT AAG CAG GTG      435
Thr Gly Gly Pro Pro Asp Pro Ser Asp Ile His Val His Lys Gln Val
              130              135              140
TGT GAG ATC ATC GAG AGC CCC CTC TTT CTG AAG TTG AAC CCT ATG ACC      483
Cys Glu Ile Ile Glu Ser Pro Leu Phe Leu Lys Leu Asn Pro Met Thr
              145              150              155
AAG CAC ACA GAT CTT CCT GTC AGC GTT TTT GAG TCT GTC ATT GAT ATA      531
Lys His Thr Asp Leu Pro Val Ser Val Phe Glu Ser Val Ile Asp Ile

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159

160 165 170 579  
 ATC AAT GGA GAG GCC ACA ATG CTG TTT GCT GAG CTG ACC TAC ACT CTG  
 Ile Asn Gly Glu Ala Thr Met Leu Phe Ala Glu Leu Thr Tyr Thr Leu  
 175 180 185 190 627  
 GCC ACA GAG GAA GCG GAA CGC ATT GGT GTA GAC CAC GTA GCC CGA ATG  
 Ala Thr Glu Glu Ala Glu Arg Ile Gly Val Asp His Val Ala Arg Met  
 195 200 205 675  
 ACA GCA ACA GGC AGT GGA GAG AAC TCC ACT GTG GCT GAA CAC CTG ATA  
 Thr Ala Thr Gly Ser Gly Glu Asn Ser Thr Val Ala Glu His Leu Ile  
 210 215 220 723  
 GCA CAG CAC AGC GCC ATC AAG ATG CTG CAC AGC CGC GTC AAG CTC ATC  
 Ala Gln His Ser Ala Ile Lys Met Leu His Ser Arg Val Lys Leu Ile  
 225 230 235 771  
 TTG GAG TAC GTC AAG GCC TCT GAA GCG GGA GAG GTC CCC TTT AAT CAT  
 Leu Glu Tyr Val Lys Ala Ser Glu Ala Gly Glu Val Pro Phe Asn His  
 240 245 250 819  
 GAG ATC CTG CGG GAG GCC TAT GCT CTG TGT CAC TGT CTC CCG GTG CTC  
 Glu Ile Leu Arg Glu Ala Tyr Ala Leu Cys His Cys Leu Pro Val Leu  
 255 260 265 270 867  
 AGC ACA GAC AAG TTC AAG ACA GAT TTT TAT GAT CAA TGC AAC GAC GTG  
 Ser Thr Asp Lys Phe Lys Thr Asp Phe Tyr Asp Gln Cys Asn Asp Val  
 275 280 285 915  
 GGG CTC ATG GCC TAC CTC GGC ACC ATC ACC AAA ACG TGC AAC ACC ATG  
 Gly Leu Met Ala Tyr Leu Gly Thr Ile Thr Lys Thr Cys Asn Thr Met  
 290 295 300 963  
 AAC CAG TTT GTG AAC AAG TTC AAT GTC CTC TAC GAC CGA CAA GGC ATC  
 Asn Gln Phe Val Asn Lys Phe Asn Val Leu Tyr Asp Arg Gln Gly Ile  
 305 310 315 1000  
 GGC AGG AGA ATG CGC GGC CTC TTT TTC TGATGAGGGT  
 Gly Arg Arg Met Arg Gly Leu Phe Phe  
 320 325 1060  
 ACTTGAAGGG CTGATGGACA GGGGTCAGGC AACTATCCCA AAGGGGAGGG CACTACACTT  
 CCTTGAGAGA AACCACTGTC ATTAATAAAA GGGGAGCAGC CCCTGAGCAC CCCTG 1115

Sequence No.: 67

Sequence length: 1721

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma

160

Cell line: HT-1080

Clone name: HP10235

Sequence characteristics

Code representing characteristics: CDS

Existence site: 6.. 1127

Characterization method: E

Sequence description

ATGTC ATG ACC CTA TGT GCC ATG CTG CCC CTG CTG TTA TTC ACC TAC CTC	50
Met Thr Leu Cys Ala Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu	
1 5 10 15	
AAC TCC TTC CTG CAT CAG AGG ATC CCC CAG TCC GTA CGG ATC CTG GGC	98
Asn Ser Phe Leu His Gln Arg Ile Pro Gln Ser Val Arg Ile Leu Gly	
20 25 30	
AGC CTG GTG GCC ATC CTG CTG GTG TTT CTG ATC ACT GCC ATC CTG GTG	146
Ser Leu Val Ala Ile Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val	
35 40 45	
AAG GTG CAG CTG GAT GCT CTG CCC TTC TTT GTC ATC ACC ATG ATC AAG	194
Lys Val Gln Leu Asp Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys	
50 55 60	
ATC GTG CTC ATT AAT TCA TTT GGT GCC ATC CTG CAG GGC AGC CTG TTT	242
Ile Val Leu Ile Asn Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe	
65 70 75	
GGT CTG GCT GGC CTT CTG CCT GCC AGC TAC ACG GCC CCC ATC ATG AGT	290
Gly Leu Ala Gly Leu Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser	
80 85 90 95	
GGC CAG GGC CTA GCA GGC TTC TTT GCC TCC GTG GCC ATG ATC TGC GCT	338
Gly Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala	
100 105 110	
ATT GCC AGT GGC TCG GAG CTA TCA GAA AGT GCC TTC GGC TAC TTT ATC	386
Ile Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile	
115 120 125	
ACA GCC TGT GCT GTT ATC ATT TTG ACC ATC ATC TGT TAC CTG GGC CTG	434
Thr Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu	
130 135 140	
CCC CGC CTG GAA TTC TAC CGC TAC TAC CAG CAG CTC AAG CTT GAA GGA	482
Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly	
145 150 155	
CCC GGG GAG CAG GAG ACC AAG TTG GAC CTC ATT AGC AAA GGA GAG GAG	530
Pro Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu	
160 165 170 175	
CCA AGA GCA GGC AAA GAG GAA TCT GGA GTT TCA GTC TCC AAC TCT CAG	578
Pro Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln	
180 185 190	

161

CCC ACC AAT GAA AGC CAC TCT ATC AAA GCC ATC CTG AAA AAT ATC TCA	626
Pro Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser	
195 200 205	
GTC CTG GCT TTC TCT GTC TGC TTC ATC TTC ACT ATC ACC ATT GGG ATG	674
Val Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met	
210 215 220	
TTT CCA GCC GTG ACT GTT GAG GTC AAG TCC AGC ATC GCA GGC AGC AGC	722
Phe Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser	
225 230 235	
ACC TGG GAA CGT TAC TTC ATT CCT GTG TCC TGT TTC TTG ACT TTC AAT	770
Thr Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn	
240 245 250 255	
ATC TTT GAC TGG TTG GGC CGG AGC CTC ACA GCT GTA TTC ATG TGG CCT	818
Ile Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro	
260 265 270	
GGG AAG GAC AGC CGC TGG CTG CCA AGC CTG GTG CTG GCC CGG CTG GTG	866
Gly Lys Asp Ser Arg Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val	
275 280 285	
TTT GTG CCA CTG CTG CTG CTG TGC AAC ATT AAG CCC CGC CGC TAC CTG	914
Phe Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu	
290 295 300	
ACT GTG GTC TTC GAG CAC GAT GCC TGG TTC ATC TTC TTC ATG GCT GCC	962
Thr Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala	
305 310 315	
TTT GCC TTC TCC AAC GGC TAC CTC GCC AGC CTC TGC ATG TGC TTC GGG	1010
Phe Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly	
320 325 330 335	
CCC AAG AAA GTG AAG CCA GCT GAG GCA GAG ACC GCA GGA GCC ATC ATG	1058
Pro Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met	
340 345 350	
GCC TTC TTC CTG TGT CTG GGT CTG GCA CTG GGG GCT GTT TTC TCC TTC	1106
Ala Phe Phe Leu Cys Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe	
355 360 365	
CTG TTC CGG GCA ATT GTG TGACAAAGGA TGGACAGAAG GACTGC	1150
Leu Phe Arg Ala Ile Val	
370	
CTGCCTCCCT CCCTGTCTGC CTCCTGCCCC TTCCTTCTGC CAGGGGTGAT CCTGAGTGGT	1210
CTGGCGGTTT TTTCTTCTAA CTGACTTCTG CTTTCCACGG CGTGTGCTGG GCCCGGATCT	1270
CCAGGCCCTG GGGAGGGAGC CTCTGGACGG ACAGTGGGGA CATTGTGGGT TTGGGGCTCA	1330
GAGTCGAGGG ACGGGGTGTA GCCTCGGCAT TTGCTTGAGT TTCTCCACTC TTGGCTCTGA	1390
CTGATCCCTG CTTGTGCAGG CCAGTGGAGG CTCTTGGGCT TGGAGAACAC GTGTGTCTCT	1450
GTGTATGTGT CTGTGTGTCT GCGTCCGTGT CTGTCAGACT GTCTGCCTGT CCTGGGGTGG	1510
CTAGGAGCTG GGTCTGACCG TTGTATGGTT TGACCTGATA TACTCCATTC TCCCCTGCGC	1570
CTCCTCTCT GTGTTCTCTC CATGTCCCC TCCCAACTCC CCATGCCCAG TTCTTACCCA	1630

162

TCATGCACCC TGTACAGTTG CCACGTTACT GCCTTTTTTA AAAATATATT TGACAGAAAC 1690  
 CAGGTGCCTT CAGAGGCTCT CTGATTTAAA T 1721

Sequence No.: 68  
 Sequence length: 1504  
 Sequence type: Nucleic acid  
 Strandedness: Double  
 Topology: Linear  
 Sequence kind: cDNA to mRNA  
 Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10297

Sequence characteristics

Code representing characteristics: CDS

Existence site: 63.. 614

Characterization method: E

Sequence description

CTTTTGCGGC TGCAGCGGC TTGTAGGTGT CCGGCTTTC TGGCCCAGCA AGCCTGATAA 60  
 GC ATG AAG CTC TTA TCT TTG GTG GCT GTG GTC GGG TGT TTG CTG GTG 107  
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
 1 5 10 15  
 CCC CCA GCT GAA GCC AAC AAG AGT TCT GAA GAT ATC CGG TGC AAA TGC 155  
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys  
 20 25 30  
 ATC TGT CCA CCT TAT AGA AAC ATC AGT GGG CAC ATT TAC AAC CAG AAT 203  
 Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn  
 35 40 45  
 GTA TCC CAG AAG GAC TGC AAC TGC CTG CAC GTG GTG GAG CCC ATG CCA 251  
 Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro  
 50 55 60  
 GTG CCT GGC CAT GAC GTG GAG GCC TAC TGC CTG CTG TGC GAG TGC AGG 299  
 Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg  
 65 70 75  
 TAC GAG GAG CGC AGC ACC ACC ACC ATC AAG GTC ATC ATT GTC ATC TAC 347  
 Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr  
 80 85 90 95  
 CTG TCC GTG GTG GGT GCC CTG TTG CTC TAC ATG GCC TTC CTG ATG CTG 395  
 Leu Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu  
 100 105 110  
 GTG GAC CCT CTG ATC CGA AAG CCG GAT GCA TAC ACT GAG CAA CTG CAC 443  
 Val Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His

163

115	120	125	491
AAT GAG GAG GAG AAT GAG GAT GCT CGC TCT ATG GCA GCA GCT GCT GCA			
Asn Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala			
130	135	140	539
TCC CTC GGG GGA CCC CGA GCA AAC ACA GTC CTG GAG CGT GTG GAA GGT			
Ser Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly			
145	150	155	587
GCC CAG CAG CGG TGG AAG CTG CAG GTG CAG GAG CAG CGG AAG ACA GTC			
Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val			
160	165	170	640
TTC GAT CGG CAC AAG ATG CTC AGC TAGATGGGCT GGTGTGGTTG GGTCAAGGC			
Phe Asp Arg His Lys Met Leu Ser			
180			
CCCAACACCA TGGCTGCCAG CTTCCAGGCT GGACAAAGCA GGGGGCTACT TCTCCCTTCC			700
CTCGGTTCCA GTCTTCCCTT TAAAAGCCTG TGGCATTTTT CCTCCTTCTC CCTAACTTTA			760
GAAATGTTGT ACTTGGCTAT TTTGATTAGG GAAGAGGGAT GTGGTCTCTG ATCTCTGTTG			820
TCTTCTTGGG TCTTTGGGGT TGAAGGGAGG GGGAAGGCAG GCCAGAAGGG AATGGAGACA			880
TTCGAGGCGG CCTCAGGAGT GGATGCCATC TGTCTCTCCT GGCTCCACTC TTGCCGCCTT			940
CCAGCTCTGA GTCTTGGGAA TGTTGTTACC CTTGGAAGAT AAAGCTGGGT CTTCAGGAAC			1000
TCAGTGTCTG GGAGGAAAGC ATGGCCCAGC ATTCAGCATG TGTTCCTTTC TGCAGTGGTT			1060
CTTATCACCA CCTCCCTCCC AGCCCCAGCG CCTCAGCCCC AGCCCCAGCT CCAGCCCTGA			1120
GGACAGCTCT GATGGGAGAG CTGGGCCCCC TGAGCCCACT GGGTCTTCAG GGTGCACTGG			1180
AAGCTGGTGT TCGCTGTCCC CTGTGCACTT CTCGCACTGG GGCATGGAGT GCCCATGCAT			1240
ACTCTGCTGC CGGTCCCCCT ACCTGCACTT GAGGGGTCTG GGCAGTCCCT CCTCTCCCCA			1300
GTGTCCACAG TCACTGAGCC AGACGGTCGG TTGGAACATG AGACTCGAGG CTGAGCGTGG			1360
ATCTGAACAC CACAGCCCCT GTACTTGGGT TGCCTCTTGT CCCTGAACTT CGTTGTACCA			1420
GTGCATGGAG AGAAAATTTT GTCCTCTTGT CTTAGAGTTG TGTGTAAATC AAGGAAGCCA			1480
TCATTAAATT GTTTATTTC TCTC			1504

Sequence No.: 69

Sequence length: 532

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10299

Sequence characteristics

Code representing characteristics: CDS

Existence site: 93.. 443

Characterization method: E



## Sequence description

GCTCTCTGGT AAAGGCGTGC AGGTGTTGGC CGCGGCCTCT GAGCTGGGAT GAGCCGTGCT 60  
 CCCGGTGGAA GCAAGGGAGC CCAGCCGGAG CC ATG GCC AGT ACA GTG GTA GCA 113  
 Met Ala Ser Thr Val Val Ala  
 1 5  
 GTT GGA CTG ACC ATT GCT GCT GCA GGA TTT GCA GGC CGT TAC GTT TTG 161  
 Val Gly Leu Thr Ile Ala Ala Ala Gly Phe Ala Gly Arg Tyr Val Leu  
 10 15 20  
 CAA GCC ATG AAG CAT ATG GAG CCT CAA GTA AAA CAA GTT TTT CAA AGC 209  
 Gln Ala Met Lys His Met Glu Pro Gln Val Lys Gln Val Phe Gln Ser  
 25 30 35  
 CTA CCA AAA TCT GCC TTC AGT GGT GGC TAT TAT AGA GGT GGG TTT GAA 257  
 Leu Pro Lys Ser Ala Phe Ser Gly Gly Tyr Tyr Arg Gly Gly Phe Glu  
 40 45 50 55  
 CCC AAA ATG ACA AAA CGG GAA GCA GCA TTA ATA CTA GGT GTA AGC CCT 305  
 Pro Lys Met Thr Lys Arg Glu Ala Ala Leu Ile Leu Gly Val Ser Pro  
 60 65 70  
 ACT GCC AAT AAA GGG AAA ATA AGA GAT GCT CAT CGA CGA ATT ATG CTT 353  
 Thr Ala Asn Lys Gly Lys Ile Arg Asp Ala His Arg Arg Ile Met Leu  
 75 80 85  
 TTA AAT CAT CCT GAC AAA GGA GGA TCT CCT TAT ATA GCA GCC AAA ATC 401  
 Leu Asn His Pro Asp Lys Gly Gly Ser Pro Tyr Ile Ala Ala Lys Ile  
 90 95 100  
 AAT GAA GCT AAA GAT TTA CTA GAA GGT CAA GCT AAA AAA TGAAGTAAAT 450  
 Asn Glu Ala Lys Asp Leu Leu Glu Gly Gln Ala Lys Lys  
 105 110 115  
 GTATGATGAA TTTTAAGTTC GTATTAGTTT ATGTATATGA GTACTAAGTT TTTATAATAA 510  
 AATGCCTCAG AGCTACAATT TT 532

Sequence No.: 70

Sequence length: 662

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10301

Sequence characteristics

165

Code representing characteristics: CDS

Existence site: 92.. 550

Characterization method: E

Sequence description

TCTAGCCCCG CCCCAGGCGA GGGCGCCGCA CCCACACCGC GCTGCGCAGT TTTGTTCTGC 60  
 TCCAGCTGTT CGAAGGTGAT CCAGACGCAA G ATG GCT GTC CTC TCT AAG GAA 112  
 Met Ala Val Leu Ser Lys Glu  
 1 5  
 TAT GGT TTT GTG CTT CTA ACT GGT GCT GCC AGC TTT ATA ATG GTG GCC 160  
 Tyr Gly Phe Val Leu Leu Thr Gly Ala Ala Ser Phe Ile Met Val Ala  
 10 15 20  
 CAC CTA GCC ATC AAT GTT TCC AAG GCC CGC AAG AAG TAC AAA GTG GAG 208  
 His Leu Ala Ile Asn Val Ser Lys Ala Arg Lys Lys Tyr Lys Val Glu  
 25 30 35  
 TAT CCT ATC ATG TAC AGC ACG GAC CCT GAA AAT GGG CAC ATC TTC AAC 256  
 Tyr Pro Ile Met Tyr Ser Thr Asp Pro Glu Asn Gly His Ile Phe Asn  
 40 45 50 55  
 TGC ATT CAG CGA GCC CAC CAG AAC ACG TTG GAA GTG TAT CCT CCC TTC 304  
 Cys Ile Gln Arg Ala His Gln Asn Thr Leu Glu Val Tyr Pro Pro Phe  
 60 65 70  
 TTA TTT TTT CTA GCT GTT GGA GGT GTT TAC CAC CCG CGT ATA GCT TCT 352  
 Leu Phe Phe Leu Ala Val Gly Gly Val Tyr His Pro Arg Ile Ala Ser  
 75 80 85  
 GGC CTG GGC TTG GCC TGG ATT GTT GGA CGA GTT CTT TAT GCT TAT GGC 400  
 Gly Leu Gly Leu Ala Trp Ile Val Gly Arg Val Leu Tyr Ala Tyr Gly  
 90 95 100  
 TAT TAC ACG GGA GAA CCC AGC AAG CGT AGT CGA GGA GCC CTG GGG TCC 448  
 Tyr Tyr Thr Gly Glu Pro Ser Lys Arg Ser Arg Gly Ala Leu Gly Ser  
 105 110 115  
 ATC GCC CTC CTG GGC TTG GTG GGC ACA ACT GTG TGC TCT GCT TTC CAG 496  
 Ile Ala Leu Leu Gly Leu Val Gly Thr Thr Val Cys Ser Ala Phe Gln  
 120 125 130 135  
 CAT CTT GGT TGG GTT AAA AGT GGC TTG GGC AGT GGA CCC AAA TGC TGC 544  
 His Leu Gly Trp Val Lys Ser Gly Leu Gly Ser Gly Pro Lys Cys Cys  
 140 145 150  
 CAT TAAAGAATTA TAGGGGTTTA AAAACTCTCA TTCATTTTAA ATG 590  
 His  
 ACTTACCTTT ATTTCCAGTT ACATTTTTTT TCTAAATATA ATAAAACTT ACCTGGCATC 650  
 AGCCTCATAC CT 662

Sequence No.: 71

Sequence length: 2373  
 Sequence type: Nucleic acid  
 Strandedness: Double  
 Topology: Linear  
 Sequence kind: cDNA to mRNA  
 Original source:

Organism species: *Homo sapiens*

Cell kind: Liver

Clone name: HP10302

Sequence characteristics

Code representing characteristics: CDS

Existence site: 134.. 1813

Characterization method: E

Sequence description

GAAGACCCCA GCGCCGGCGC GGCTCAGGGC TGGGCCACG GGA	CGCTCCGGA CGCGCCGCGA	60
AAGCGTTGCG CTCCCGGAGG CGTCCGCAGC TGCTGGCTGC TCATTG	CCCG GTGACCGGAG	120
GCTCGGGGCC AGC ATG GCC CCC ACG CTG CAA CAG GCG TAC	CGG AGG CGC	169
Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg		
1 5 10		
TGG TGG ATG GCC TGC ACG GCT GTG CTG GAG AAC CTC TTC	TCT GCT	217
Trp Trp Met Ala Cys Thr Ala Val Leu Glu Asn Leu Phe Phe	Ser Ala	
15 20 25		
GTA CTC CTG GGC TGG GGC TCC CTG TTG ATC ATT CTG AAG	AAC GAG GGC	265
Val Leu Leu Gly Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn	Glu Gly	
30 35 40		
TTC TAT TCC AGC ACG TGC CCA GCT GAG AGC AGC ACC AAC	ACC CAG	313
Phe Tyr Ser Ser Thr Cys Pro Ala Glu Ser Ser Thr Asn	Thr Thr Gln	
45 50 55 60		
GAT GAG CAG CGC AGG TGG CCA GGC TGT GAC CAG CAG GAC	GAG ATG CTC	361
Asp Glu Gln Arg Arg Trp Pro Gly Cys Asp Gln Gln Asp	Glu Met Leu	
65 70 75		
AAC CTG GGC TTC ACC ATT GGT TCC TTC GTG CTC AGC GCC	ACC ACC CTG	409
Asn Leu Gly Phe Thr Ile Gly Ser Phe Val Leu Ser Ala	Thr Thr Leu	
80 85 90		
CCA CTG GGG ATC CTC ATG GAC CGC TTT GGC CCC CGA CCC	GTG CGG CTG	457
Pro Leu Gly Ile Leu Met Asp Arg Phe Gly Pro Arg Pro	Val Arg Leu	
95 100 105		
GTT GGC AGT GCC TGC TTC ACT GCG TCC TGC ACC CTC	ATG GCC CTG GCC	505
Val Gly Ser Ala Cys Phe Thr Ala Ser Cys Thr Leu Met	Ala Leu Ala	
110 115 120		
TCC CGG GAC GTG GAA GCT CTG TCT CCG TTG ATA TTC	CTG GCG CTG TCC	553
Ser Arg Asp Val Glu Ala Leu Ser Pro Leu Ile Phe Leu	Ala Leu Ser	
125 130 135 140		

167

CTG AAT GGC TTT GGT GGC ATC TGC CTA ACG TTC ACT TCA CTC ACG CTG 601  
 Leu Asn Gly Phe Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu  
 145 150 155  
 CCC AAC ATG TTT GGG AAC CTG CGC TCC ACG TTA ATG GCC CTC ATG ATT 649  
 Pro Asn Met Phe Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile  
 160 165 170  
 GGC TCT TAC GCC TCT TCT GCC ATT ACG TTC CCA GGA ATC AAG CTG ATC 697  
 Gly Ser Tyr Ala Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile  
 175 180 185  
 TAC GAT GCC GGT GTG GCC TTC GTG GTC ATC ATG TTC ACC TGG TCT GGC 745  
 Tyr Asp Ala Gly Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly  
 190 195 200  
 CTG GCC TGC CTT ATC TTT CTG AAC TGC ACC CTC AAC TGG CCC ATC GAA 793  
 Leu Ala Cys Leu Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu  
 205 210 215 220  
 GCC TTT CCT GCC CCT GAG GAA GTC AAT TAC ACG AAG AAG ATC AAG CTG 841  
 Ala Phe Pro Ala Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu  
 225 230 235  
 AGT GGG CTG GCC CTG GAC CAC AAG GTG ACA GGT GAC CTC TTC TAC ACC 889  
 Ser Gly Leu Ala Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr  
 240 245 250  
 CAT GTG ACC ACC ATG GGC CAG AGG CTC AGC CAG AAG GCC CCC AGC CTG 937  
 His Val Thr Thr Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu  
 255 260 265  
 GAG GAC GGT TCG GAT GCC TTC ATG TCA CCC CAG GAT GTT CGG GGC ACC 985  
 Glu Asp Gly Ser Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr  
 270 275 280  
 TCA GAA AAC CTT CCT GAG AGG TCT GTC CCC TTA CGC AAG AGC CTC TGC 1033  
 Ser Glu Asn Leu Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys  
 285 290 295 300  
 TCC CCC ACT TTC CTG TGG AGC CTC CTC ACC ATG GGC ATG ACC CAG CTG 1081  
 Ser Pro Thr Phe Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu  
 305 310 315  
 CGG ATC ATC TTC TAC ATG GCT GCT GTG AAC AAG ATG CTG GAG TAC CTT 1129  
 Arg Ile Ile Phe Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu  
 320 325 330  
 GTG ACT GGT GGC CAG GAG CAT GAG ACA AAT GAA CAG CAA CAA AAG GTG 1177  
 Val Thr Gly Gly Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val  
 335 340 345  
 GCA GAG ACA GTT GGG TTC TAC TCC TCC GTC TTC GGG GCC ATG CAG CTG 1225  
 Ala Glu Thr Val Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu  
 350 355 360  
 TTG TGC CTT CTC ACC TGC CCC CTC ATT GGC TAC ATC ATG GAC TGG CGG 1273  
 Leu Cys Leu Leu Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg

168

365	370	375	380	
ATC AAG GAC TGC GTG GAC GCC CCA ACT CAG GGC ACT GTC CTC GGA GAT				1321
Ile Lys Asp Cys Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp				
	385	390	395	
GCC AGG GAC GGG GTT GCT ACC AAA TCC ATC AGA CCA CGC TAC TGC AAG				1369
Ala Arg Asp Gly Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys				
	400	405	410	
ATC CAA AAG CTC ACC AAT GCC ATC AGT GCC TTC ACC CTG ACC AAC CTG				1417
Ile Gln Lys Leu Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu				
	415	420	425	
CTG CTT GTG GGT TTT GGC ATC ACC TGT CTC ATC AAC AAC TTA CAC CTC				1465
Leu Leu Val Gly Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu				
	430	435	440	
CAG TTT GTG ACC TTT GTC CTG CAC ACC ATT GTT CGA GGT TTC TTC CAC				1513
Gln Phe Val Thr Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His				
	445	450	455	
TCA GCC TGT GGG AGT CTC TAT GCT GCA GTG TTC CCA TCC AAC CAC TTT				1561
Ser Ala Cys Gly Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe				
	465	470	475	
GGG ACG CTG ACA GGC CTG CAG TCC CTC ATC AGT GCT GTG TTC GCC TTG				1609
Gly Thr Leu Thr Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu				
	480	485	490	
CTT CAG CAG CCA CTT TTC ATG GCG ATG GTG GGA CCC CTG AAA GGA GAG				1657
Leu Gln Gln Pro Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu				
	495	500	505	
CCC TTC TGG GTG AAT CTG GGC CTC CTG CTA TTC TCA CTC CTG GGA TTC				1705
Pro Phe Trp Val Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe				
	510	515	520	
CTG TTG CCT TCC TAC CTC TTC TAT TAC CGT GCC CGG CTC CAG CAG GAG				1753
Leu Leu Pro Ser Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu				
	525	530	535	
TAC GCC GCC AAT GGG ATG GGC CCA CTG AAG GTG CTT AGC GGC TCT GAG				1801
Tyr Ala Ala Asn Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu				
	545	550	555	
GTG ACC GCA TAGACTTCTC AGACCAAGGG ACCTGGATGA				1840
Val Thr Ala				
CAGGCAATCA AGGCCTGAGC AACC AAAAGG AGTGCCCAT ATGGCTTTTC TACCTGTAAC				1900
ATGCACATAG AGCCATGGCC GTAGATTTAT AAATACCAAG AGAAGTTCTA TTTTGTAAA				1960
GACTGCAAAA AGGAGGAAAA AAAAACCTTC AAAAACGCC CTAAGTCAA CGCTCCATTG				2020
ACTGAAGACA GTCCCTATCC TAGAGGGGTT GAGCCTTCTT CCTCCTTGGG TTGGAGGAGA				2080
CCAGGGTGCC TCTTATCTCC TTCTAGCGGT CTGCCTCTG GTACCTCTG GGGGGATCGG				2140
CAAACAGGCT ACCCCTGAGG TCCCATGTGC CATGAGTGTG CACACATGCA TGTGTCTGTG				2200
TATGTGTGAA TGTGAGAGAG ACACAGCCCT CCTTTCAGAA GGAAAGGGGC CTGAGGTGCC				2260

AGCTGTGTCC TGGGTTAGGG GTTGGGGGTC GGCCCTTCC AGGGCCAGGA GGGCAGGTTC 2320  
 CCTCTCTGGT GCTGCTGCTT GCAAGTCTTA GAGGAAATAA AAAGGGAAGT GAG 2373

Sequence No.: 72

Sequence length: 1316

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Osteosarcoma

Cell line: U-2 OS

Clone name: HP10304

Sequence characteristics

Code representing characteristics: CDS

Existence site: 11.. 1003

Characterization method: E

Sequence description

GTGTGTTCCAAG ATG GAG GGC GCT CCA CCG GGG TCG CTC GCC CTC CGG CTC 49  
 Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu  
 1 5 10  
 CTG CTG TTC GTG GCG CTA CCC GCC TCC GGC TGG CTG ACG ACG GGC GCC 97  
 Leu Leu Phe Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala  
 15 20 25  
 CCC GAG CCG CCG CCG CTG TCC GGA GCC CCA CAG GAC GGC ATC AGA ATT 145  
 Pro Glu Pro Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile  
 30 35 40 45  
 AAT GTA ACT ACA CTG AAA GAT GAT GGG GAC ATA TCT AAA CAG CAG GTT 193  
 Asn Val Thr Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln Val  
 50 55 60  
 GTT CTT AAC ATA ACC TAT GAG AGT GGA CAG GTG TAT GTA AAT GAC TTA 241  
 Val Leu Asn Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn Asp Leu  
 65 70 75  
 CCT GTA AAT AGT GGT GTA ACC CGA ATA AGC TGT CAG ACT TTG ATA GTG 289  
 Pro Val Asn Ser Gly Val Thr Arg Ile Ser Cys Gln Thr Leu Ile Val  
 80 85 90  
 AAG AAT GAA AAT CTT GAA AAT TTG GAG GAA AAA GAA TAT TTT GGA ATT 337  
 Lys Asn Glu Asn Leu Glu Asn Leu Glu Glu Lys Glu Tyr Phe Gly Ile  
 95 100 105  
 GTC AGT GTA AGG ATT TTA GTT CAT GAG TGG CCT ATG ACA TCT GGT TCC 385  
 Val Ser Val Arg Ile Leu Val His Glu Trp Pro Met Thr Ser Gly Ser

170

110	115	120	125	
AGT TTG CAA CTA ATT GTC ATT CAA GAA GAG GTA GTA GAG ATT GAT GGA				433
Ser Leu Gln Leu Ile Val Ile Gln Glu Glu Val Val Glu Ile Asp Gly				
	130	135	140	
AAA CAA GTT CAG CAA AAG GAT GTC ACT GAA ATT GAT ATT TTA GTT AAG				481
Lys Gln Val Gln Gln Lys Asp Val Thr Glu Ile Asp Ile Leu Val Lys				
	145	150	155	
AAC CGG GGA GTA CTC AGA CAT TCA AAC TAT ACC CTC CCT TTG GAA GAA				529
Asn Arg Gly Val Leu Arg His Ser Asn Tyr Thr Leu Pro Leu Glu Glu				
	160	165	170	
AGC ATG CTC TAC TCT ATT TCT CGA GAC AGT GAC ATT TTA TTT ACC CTT				577
Ser Met Leu Tyr Ser Ile Ser Arg Asp Ser Asp Ile Leu Phe Thr Leu				
	175	180	185	
CCT AAC CTC TCC AAA AAA GAA AGT GTT AGT TCA CTG CAA ACC ACT AGC				625
Pro Asn Leu Ser Lys Lys Glu Ser Val Ser Ser Leu Gln Thr Thr Ser				
	190	195	200	205
CAG TAT CTT ATC AGG AAT GTG GAA ACC ACT GTA GAT GAA GAT GTT TTA				673
Gln Tyr Leu Ile Arg Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu				
	210	215	220	
CCT GGC AAG TTA CCT GAA ACT CCT CTC AGA GCA GAG CCG CCA TCT TCA				721
Pro Gly Lys Leu Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser				
	225	230	235	
TAT AAG GTA ATG TGT CAG TGG ATG GAA AAG TTT AGA AAA GAT CTG TGT				769
Tyr Lys Val Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys				
	240	245	250	
AGG TTC TGG AGC AAC GTT TTC CCA GTA TTC TTT CAG TTT TTG AAC ATC				817
Arg Phe Trp Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile				
	255	260	265	
ATG GTG GTT GGA ATT ACA GGA GCA GCT GTG GTA ATA ACC ATC TTA AAG				865
Met Val Val Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys				
	270	275	280	285
GTG TTT TTC CCA GTT TCT GAA TAC AAA GGA ATT CTT CAG TTG GAT AAA				913
Val Phe Phe Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp Lys				
	290	295	300	
GTG GAC GTC ATA CCT GTG ACA GCT ATC AAC TTA TAT CCA GAT GGT CCA				961
Val Asp Val Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp Gly Pro				
	305	310	315	
GAG AAA AGA GCT GAA AAC CTT GAA GAT AAA ACA TGT ATT TAAACGCCA				1010
Glu Lys Arg Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile				
	320	325	330	
TCTCATATCA TGGACTCCGA AGTAGCCTGT TGCCTCCAAA TTTGCCACTT GAATATAATT				1070
TTCTTTAAAT CGTTAAGAAT CAGTTTATAC ACTAGAGAAA TTGCTAAACT CTAAGACTGC				1130
CTGAAAATTG ACCTTTACAG TGCCAAGTTA AAGTTTACCT TATTCTCGGC CGGGTGCAGT				1190
GGCTCATGCC TGTAATCCCA GGAAGTTGGG AGGCCAATGC GGGCGGATCA CGAGGTCAGA				1250

171

TCAAGACCAT CCTGCCAACA TGGTGAACCT CTGTCTCTAC TAAAAAAAAT AAAAAAGTTA 1310  
GCTGGG 1316

Sequence No.: 73  
Sequence length: 893  
Sequence type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Sequence kind: cDNA to mRNA  
Original source:

Organism species: *Homo sapiens*

Cell kind: Osteosarcoma

Cell line: U-2 OS

Clone name: HP10305

Sequence characteristics

Code representing characteristics: CDS

Existence site: 110.. 436

Characterization method: E

Sequence description

ATCGCGGAGT CGGTGCTTTA GTACCGCGCT GGCACCTTTA CTCTCGCCGG CCGCGCGAAC 60  
CCGTTTGAGC TCGGTATCCT AGTGCACAGC CCTTGCAAGC GACGGCGCC ATG AGT CTG 118  
Met Ser Leu

1  
ACT TCC AGT TCC AGC GTA CGA GTT GAA TGG ATC GCA GCA GTT ACC ATT 166  
Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr Ile  
5 10 15  
GCT GCT GGG ACA GCT GCA ATT GGT TAT CTA GCT TAC AAA AGA TTT TAT 214  
Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe Tyr  
20 25 30 35  
GTT AAA GAT CAT CGA AAT AAA GCT ATG ATA AAC CTT CAC ATC CAG AAA 262  
Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln Lys  
40 45 50  
GAC AAC CCC AAG ATA GTA CAT GCT TTT GAC ATG GAG GAT TTG GGA GAT 310  
Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Leu Gly Asp  
55 60 65  
AAA GCT GTG TAC TGC CGT TGT TGG AGG TCC AAA AAG TTC CCA TTC TGT 358  
Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe Cys  
70 75 80  
GAT GGG GCT CAC ACA AAA CAT AAC GAA GAG ACT GGA GAC AAT GTG GGC 406  
Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp Asn Val Gly  
85 90 95  
CCT CTG ATC ATC AAG AAA AAA GAA ACT TAAATGGACA CTTTGA 450



172

Pro Leu Ile Ile Lys Lys Lys Glu Thr

100	105		510
TGCTGCAAAT	CAGCTTGTCTG	TGAAGTTACC	TGATTGTTTA
			ATTAGAATGA
			CTACCACCTC
			570
TGTCTGATTC	ACCTTCGCTG	GATTCTAAAT	GTGGTATATT
			GCAAACTGCA
			GCTTTCACAT
			630
TTATGGCATT	TGTCTTGTG	AAACATCGTG	GTGCACATTT
			GTTTAAACAA
			AAAAAAAAAA
			690
AAAAAGGAAA	AACCAACCTC	ATGGCCTGTG	GGTTATTTTG
			GTCTTGTAAG
			GATCCATTTT
			750
TTTAAAATAC	TGACATATAG	AGTTGTACCT	TATATAGAAT
			ATAGTTGTAT
			CTTGAAGTCA
			810
ACATATTAAT	TTATTCTCAA	AATTATGTAT	TTGCAGATTG
			TACTTGTAAG
			TTTCAAAGAA
			870
AAATTACCAT	CTTTTCATAT	TGACCTGGAA	ACTAAATAGG
			ATGTGATTCA
			GCTACATTAA
			893
TTTCTTAATA	CAATCTAGGA	AAG	

Sequence No.: 74

Sequence length: 690

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Osteosarcoma

Cell line: U-2 OS

Clone name: HP10306

Sequence characteristics

Code representing characteristics: CDS

Existence site: 230... 535

Characterization method: E

Sequence description

TAACAGCGCA	TGCGTGCACT	GTTGCCTCGC	CCAAAGAAGA	CTACAATCTC	CAGGGAAACC	60
TGGGGCGTCT	CGCGCAAACG	TCCATAACTG	AAAGTAGCTA	AGGCACCCCA	GCCGGAGGAA	120
GTGAGCTCTC	CTGGGGCGTG	GTTGTTTCGTG	ATCCTTGCAAT	CTGTTACTTA	GGGTCAAGGC	180
TTGGGTCTTG	CCCCGCAGAC	CCTTGGGACG	ACCCGGCCCC	AGCGCAGCT	ATG AAC CTG	238
					Met Asn Leu	

1

GAG CGA GTG	TCC AAT GAG	GAG AAA TTG	AAC CTG TGC	CGG AAG TAC	TAC TAC	286
Glu Arg Val	Ser Asn Glu	Glu Lys Leu	Asn Leu Cys	Arg Lys Tyr	Tyr Tyr	

5

10

15

CTG GGG GGG	TTT GCT TTC	CTG CCT TTT	CTC TGG TTG	GTC AAC ATC	TTC	334
Leu Gly Gly	Phe Ala Phe	Leu Pro Phe	Leu Trp Leu	Val Asn Ile	Phe	

20

25

30

35

TGG TTC TTC	CGA GAG GCC	TTC CTT GTC	CCA GCC TAC	ACA GAA CAG	AGC	382
Trp Phe Phe	Arg Glu Ala	Phe Leu Val	Pro Ala Tyr	Thr Glu Gln	Ser	

40

45

50

173

CAA ATC AAA GGC TAT GTC TGG CGC TCA GCT GTG GGC TTC CTC TTC TGG 430  
 Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp  
 55 60 65  
 GTG ATA GTG CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC TAC CGG CCC 478  
 Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro  
 70 75 80  
 CGC TGG GGT GCC CTT GGG GAC TAC CTC TCC TTC ACC ATA CCC CTG GGC 526  
 Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile Pro Leu Gly  
 85 90 95  
 ACC CCC TGACAACTTC TGCACATACT GGGGCCCTGC TTATTCTCCC AGGACAGG 580  
 Thr Pro  
 100  
 CTCCTTAAAG CAGAGGAGCC TGTCCTGGGA GCCCCTTCTC AAACCTCCTAA GACTTGTTTT 640  
 CATGTCCCAC GTTCTCTGCT GACATCCCCC AATAAAGGAC CCTAACTTTC 690

Sequence No.: 75

Sequence length: 2186

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

Organism species: *Homo sapiens*

Cell kind: Epidermoid carcinoma

Cell line: KB

Clone name: HP10328

Sequence characteristics

Code representing characteristics: CDS

Existence site: 118.. 1236

Characterization method: E

Sequence description

ACTCTTTCTT CGGCTCGCGA GCTGAGAGGA GCAGGTAGAG GGGCAGAGGC GGGACTGTCC 60  
 TCTGGGGGAG CCGCCCAGGA GGCTCCTCAG GCCGACCCCA GACCCTGGCT GGCCAGG 117  
 ATG AAG TAT CTC CGG CAC CGG CGG CCC AAT GCC ACC CTC ATT CTG GCC 165  
 Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala  
 1 5 10 15  
 ATC GGC GCT TTC ACC CTC CTC CTC TTC AGT CTG CTA GTG TCA CCA CCC 213  
 Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro  
 20 25 30  
 ACC TGC AAG GTC CAG GAG CAG CCA CCG GCG ATC CCC GAG GCC CTG GCC 261  
 Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala  
 35 40 45

174

TGG CCC ACT CCA CCC ACC CGC CCA GCC CCG GCC CCG TGC CAT GCC AAC 309  
 Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn  
 50 55 60  
 ACC TCT ATG GTC ACC CAC CCG GAC TTC GCC ACG CAG CCG CAG CAC GTT 357  
 Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val  
 65 70 75 80  
 CAG AAC TTC CTC CTG TAC AGA CAC TGC CGC CAC TTT CCC CTG CTG CAG 405  
 Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln  
 85 90 95  
 GAC GTG CCC CCC TCT AAG TGC GCG CAG CCG GTC TTC CTG CTG CTG GTG 453  
 Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val  
 100 105 110  
 ATC AAG TCC TCC CCT AGC AAC TAT GTG CGC CGC GAG CTG CTG CGG CGC 501  
 Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg  
 115 120 125  
 ACG TGG GGC CGC GAG CGC AAG GTA CCG GGT TTG CAG CTG CGC CTC CTC 549  
 Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu Gln Leu Arg Leu Leu  
 130 135 140  
 TTC CTG GTG GGC ACA GCC TCC AAC CCG CAC GAG GCC CGC AAG GTC AAC 597  
 Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu Ala Arg Lys Val Asn  
 145 150 155 160  
 CGG CTG CTG GAG CTG GAG GCA CAG ACT CAC GGA GAC ATC CTG CAG TGG 645  
 Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly Asp Ile Leu Gln Trp  
 165 170 175  
 GAC TTC CAC GAC TCC TTC TTC AAC CTC ACG CTC AAG CAG GTC CTG TTC 693  
 Asp Phe His Asp Ser Phe Phe Asn Leu Thr Leu Lys Gln Val Leu Phe  
 180 185 190  
 TTA CAG TGG CAG GAG ACA AGG TGC GCC AAC GCC AGC TTC GTG CTC AAC 741  
 Leu Gln Trp Gln Glu Thr Arg Cys Ala Asn Ala Ser Phe Val Leu Asn  
 195 200 205  
 GGG GAT GAT GAC GTC TTT GCA CAC ACA GAC AAC ATG GTC TTC TAC CTG 789  
 Gly Asp Asp Asp Val Phe Ala His Thr Asp Asn Met Val Phe Tyr Leu  
 210 215 220  
 CAG GAC CAT GAC CCT GGC CGC CAC CTC TTC GTG GGG CAA CTG ATC CAA 837  
 Gln Asp His Asp Pro Gly Arg His Leu Phe Val Gly Gln Leu Ile Gln  
 225 230 235 240  
 AAC GTG GGC CCC ATC CGG GCT TTT TGG AGC AAG TAC TAT GTG CCA GAG 885  
 Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr Val Pro Glu  
 245 250 255  
 GTG GTG ACT CAG AAT GAG CGG TAC CCA CCC TAT TGT GGG GGT GGT GGC 933  
 Val Val Thr Gln Asn Glu Arg Tyr Pro Pro Tyr Cys Gly Gly Gly Gly  
 260 265 270  
 TTC TTG CTG TCC CGC TTC ACG GCC GCT GCC CTG CGC CGT GCT GCC CAT 981  
 Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu Arg Arg Ala Ala His

175

275	280	285	
GTC TTG GAC ATC TTC CCC ATT GAT GAT GTC TTC CTG GGT ATG TGT CTG			1029
Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe Leu Gly Met Cys Leu			
290	295	300	
GAG CTT GAG GGA CTG AAG CCT GCC TCC CAC AGC GGC ATC CGC ACG TCT			1077
Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile Arg Thr Ser			
305	310	315	320
GGC GTG CGG GCT CCA TCG CAA CAC CTG TCC TCC TTT GAC CCC TGC TTC			1125
Gly Val Arg Ala Pro Ser Gln His Leu Ser Ser Phe Asp Pro Cys Phe			
325	330	335	
TAC CGA GAC CTG CTG CTG GTG CAC CGC TTC CTA CCT TAT GAG ATG CTG			1173
Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu			
340	345	350	
CTC ATG TGG GAT GCG CTG AAC CAG CCC AAC CTC ACC TGC GGC AAT CAG			1221
Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln			
355	360	365	
ACA CAG ATC TAC TGAGTCAGCA TCAGGGTCCC CAGCCTCTGG GCTCCTG			1270
Thr Gln Ile Tyr			
370			
TTTCCATAGG AAGGGGCGAC ACCTTCCTCC CAGGAAGCTG AGACCTTTGT GGTCTGAGCA			1330
TAAGGGAGTG CCAGGGAAGG TTTGAGGTTT GATGAGTGAA TATTCTGGCT GGCGAACTCC			1390
TACACATCCT TCAAAAACCCA CCTGGTACTG TTCCAGCATC TTCCCTGGAT GGCTGGAGGA			1450
ACTCCAGAAA ATATCCATCT TCTTTTTGTG GCTGCTAATG GCAGAAGTGC CTGTGCTAGA			1510
GTTCCAACTG TGGATGCATC CGTCCCCTTT GAGTCAAAGT CTTACTTCCC TGCTCTCACC			1570
TACTCACAGA CGGGATGCTA AGCAGTGCAC CTGCAGTGGT TTAATGGCAG ATAAGCTCCG			1630
TCTGCAGTTC CAGGCCAGCC AGAACTCCT GTGTCCACAT AGAGCTGACG TGAGAAATAT			1690
CTTTAGCCC AGGAGAGAGG GGTCTGTATC TTAACCCTTT CCTGGGTCTC AGACAACTCA			1750
GAAGGTTGGG GGGATACCAG AGAGGTGGTG GAATAGGACC GCCCCCTCCT TACTTGTTGGG			1810
ATCAAATGCT GTAATGGTGG AGGTGTGGGC AGAGGAGGGA GGCAAGTGTC CTTTGAAAGT			1870
TGTGAGAGCT CAGAGTTTCT GGGGTCCTCA TTAGGAGCCC CCATCCCTGT GTTCCCCAAG			1930
AATTCAGAGA ACAGCACTGG GGCTGGAATG ATCTTTAATG GGCCCAAGGC CAACAGGCAT			1990
ATGCCTCACT ACTGCCTGGA GAAGGGAGAG ATTCAGGTCC TCCAGCAGCC TCCCTCACCC			2050
AGTATGTTTT ACAGATTACG GGGGGACCGG GTGAGCCAGT GACCCCCTGC AGCCCCCAGC			2110
TTCAGGCCTC AGTGTCTGCC AGTCAAGCTT CACAGGCATT GTGATGGGGC AGCCTTGGGG			2170
AATATAAAAT TTTGTG			2186

